

STIC-Biotech/ChemLib

179876 Search notes

From: Chan, Christina
Sent: Friday, February 17, 2006 9:09 AM
To: Sitton, Jehanne Souaya; STIC-Biotech/ChemLib
Subject: RE: rush search for an after final

Please rush. Thanks Chris

Chris Chan
TC 1600 New Hire Training Coordinator and SPE 1644
(571)-272-0841
Remsen, 3E89

RECEIVED
FEB 17 2006
(STIC)

-----Original Message-----

From: Sitton, Jehanne Souaya
Sent: Friday, February 17, 2006 8:05 AM
To: Chan, Christina
Subject: rush search for an after final

Christina,
Please forward this rush request to STIC. It's for an afterfinal.

Please perform an interference search for the following: 1) nucleotides 1-1407 of
SEQ ID NO: 1 and 2) nucleotides 11200-12800 for SEQ ID NO: 1 in application
09/673,476.

↳ this is a mistake - stic
searched 1533 base pairs
from position 11199 -

thanks,
Jehanne Sitton
Primary Examiner
Art Unit 1634
Rem-2D81 (office)
Rem-2C70 (mailbox)
571-272-0752

12732
of Seq 1

Searcher: Noble
Searcher Phone: _____
Date Searcher Picked up: 2/17/06
Date completed: 2/21/06
Searcher Prep Time: 5
Online Time: 5

Type of Search
NA# 2 AA#: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: compugen
WWW/Internet: _____
Other (Specify): _____

11

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 19, 2006, 20:22:54 ; Search time 284.179 Seconds
(without alignments)
9589.048 Million cell updates/sec

Title: US-09-673-476-1_COPY_11200_12800

Perfect score: 1533

Sequence: 1 atgttcagtcgcgaacctc.....gtcgggtgctggtgctgc 1533

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1103057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2.6/prodata/1/ina/1 COMB.seq:*
- 2: /cgn2.6/prodata/1/ina/5 COMB.seq:*
- 3: /cgn2.6/prodata/1/ina/6A COMB.seq:*
- 4: /cgn2.6/prodata/1/ina/6B COMB.seq:*
- 5: /cgn2.6/prodata/1/ina/H COMB.seq:*
- 6: /cgn2.6/prodata/1/ina/PCUS COMB.seq:*
- 7: /cgn2.6/prodata/1/ina/PP COMB.seq:*
- 8: /cgn2.6/prodata/1/ina/RE COMB.seq:*
- 9: /cgn2.6/prodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1533	100.0	12732	3	US-09-060-756-1
2	1533	100.0	12732	3	US-09-670-314-1
3	1533	100.0	4403765	3	US-09-103-840A-2
4	1533	100.0	4411529	3	US-09-103-840A-1
5	1119	73.0	1119	3	US-09-894-844-53
6	479.8	31.3	4403765	3	US-09-103-840A-2
7	478.2	31.2	4411529	3	US-09-103-840A-1
8	311	20.3	894	3	US-09-894-844-52
9	56	3.7	1236	3	US-09-894-844-127
10	56	3.7	1574	3	US-09-902-540-2466
11	56	3.7	14077	3	US-09-902-540-1109
12	54.4	3.5	9521	3	US-09-902-540-953
13	53	3.5	2067	2	US-08-713-928B-8
14	53	3.5	2155	3	US-09-191-171-4
15	53	3.5	2155	3	US-09-385-707-4
16	53	3.5	2155	3	US-09-639-696C-4
17	53	3.5	2155	3	US-09-917-254-30
18	53	3.5	6200	3	US-09-439-923-1
19	53	3.5	6200	3	US-09-711-202A-1
20	53	3.5	6200	3	US-09-711-205A-1
21	53	3.5	6200	3	US-09-993-241-1
22	51.8	3.4	58857	3	US-09-477-962-1
23	51.6	3.4	12449	3	US-09-949-016-15755
24	50.8	3.3	1344	3	US-09-252-991A-9345

ALIGNMENTS

RESULT 1

US-09-060-756-1
; Sequence 1, Application US/09060756
; Patent No. 6183957
; GENERAL INFORMATION:
; APPLICANT: Cole, Stewart
; APPLICANT: Buchrieser-Brosch, Roland
; APPLICANT: Gordon, Stephen
; APPLICANT: Billault, Alain
; TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM
; TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA
; TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA
; FILE REFERENCE: 3495-0169
; CURRENT APPLICATION NUMBER: US/09/060,756
; CURRENT FILING DATE: 1998-04-16
; NUMBER OF SEQ ID NOS: 743
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 12732
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-09-060-756-1

Query Match	100.0%	Score	1533	DB	3	Length	12732
Best Local Similarity	100.0%	Pred.	No. 0				
Matches	1533	Conservative	0	Mismatches	0	Indels	0
Gaps	0						
QY	1	ARGTTTCAGCTCCGGAACCTCGATCCCGAGGACCTGAAATCCCATCCGCGGACCCGACC	60				
Db	11200	ARGTTTCAGCTCCGGAACCTCGATCCCGAGGACCTGAAATCCCATCCGCGGACCCGACC	11259				
QY	61	GGTATCCCGCTTCCAAAGCAGCCGACATCGGCGAGCTAGTGCTTTGTCCCGGGA	120				
Db	11260	GGTATCCCGCTTCCAAAGCAGCCGACATCGGCGAGCTAGTGCTTTGTCCCGGGA	11319				
QY	121	RAGAGCTTCCAGATCCCGCGCGGAGATGACACAGGACGATTCGTACGTCGC	180				
Db	11320	RAGAGCTTCCAGATCCCGCGCGGAGATGACACAGGACGATTCGTACGTCGC	11379				
QY	181	GAGGACTCCGCTATCGTCAAGTTCCGTCGTCGAGCGAACTGTGGCGGTGAATTGT	240				
Db	11380	GAGGACTCCGCTATCGTCAAGTTCCGTCGTCGAGCGAACTGTGTGGCGGTGAATTGT	11439				
QY	241	ACCGCGCGCGGAGATTTCTGTGCCATCACTTGGTAGCCCTTCGCTCGCTCGG	300				
Db	11440	ACCGCGCGCGGAGATTTCTGTGCCATCACTTGGTAGCCCTTCGCTCGCTCGG	11499				

Sequence 9429, Ap
Sequence 9316, Ap
Sequence 193, Ap
Sequence 8, Appli
Sequence 8, Appli
Sequence 14, Appli
Sequence 8965, Ap
Sequence 957, Ap
Sequence 4013, Ap
Sequence 1, Appli
Sequence 1, Appli
Sequence 4843, Ap
Sequence 7, Appli
Sequence 26, Appli
Sequence 28, Appli
Sequence 27, Appli
Sequence 1238, Ap
Sequence 8855, Ap
Sequence 943, Ap
Sequence 12805, A
Sequence 12664, A

QY 301 TTGTGTCACATGTCAGGCTCGACAGCGCGCTCGAGCCGGAGGCGGCACACATCCACGA 360
Db |||||
11500 TTGTGTCACATGTCAGGCTCGACAGCGCGCTCGAGCCGGAGGCGGCACACATCCACGA 11559
QY 361 GCCCCTCGGGCTCGGCTCGGCGGCGAGCTTGCCCACTCGGCTCTTGAGCCGCGCG 420
Db |||||
11560 GCCCCTCGGGCTCGGCTCGGCGGCGAGCTTGCCCACTCGGCTCTTGAGCCGCGCG 11619
QY 421 CGGGTGTGCCCGCGGCTGCTGAGCGCCAGCATGCGGATCGCGGATGCGCGCGATGG 480
Db |||||
11620 CGGGTGTGCCCGCGGCTGCTGAGCGCCAGCATGCGGATCGCGGATGCGCGCGATGG 11679
QY 481 TTTCTGTCAGCGCGCGCGCCCTCGGCGCTGGAACGTTTGGCGATCTGCGCAAGATCC 540
Db |||||
11680 TTTCTGTCAGCGCGCGCGCCCTCGGCGCTGGAACGTTTGGCGATCTGCGCAAGATCC 11739
QY 541 AGTCGGCCATGACGGCGATGAGTCTCTCGCGCGCGGGGTCTCCCGGGAACAGGTGAGCA 600
Db |||||
11740 AGTCGGCCATGACGGCGATGAGTCTCTCGCGCGCGGGGTCTCCCGGGAACAGGTGAGCA 11799
QY 601 TCGGTCAAACGTGCGCGCATGCCCGGACCTCGGTCAACGAGAACTTTGGCGGGTCCA 660
Db |||||
11800 TCGGTCAAACGTGCGCGCATGCCCGGACCTCGGTCAACGAGAACTTTGGCGGGTCCA 11859
QY 661 CCACCTGTTGTGCCACATGCTTGGCGTGGGGCGGATACAGCGCATGTTGTCGGCA 720
Db |||||
11860 CCACCTGTTGTGCCACATGCTTGGCGTGGGGCGGATACAGCGCATGTTGTCGGCA 11919
QY 721 ACATGCGGATGTCGCATCACCGGTGCGGACGTGACAGTACAGTCCAGGGGATGA 780
Db |||||
11920 ACATGCGGATGTCGCATCACCGGTGCGGACGTGACAGTACAGTCCAGGGGATGA 11979
QY 781 CGTGCGCAGGAATGTCGTAGCGTTCAGCGCAGCGTACACGCGCGAGTTGGTCTGGA 840
Db |||||
11980 CGTGCGCAGGAATGTCGTAGCGTTCAGCGCAGCGTACACGCGCGAGTTGGTCTGGA 12039
QY 841 TCAAGTTCAATCAAGATCAACGATCAAGGCTCAAGTTGCCCGCGCACCCGAAACCGGGGGA 900
Db |||||
12040 TCAAGTTCAATCAAGATCAACGATCAAGGCTCAAGTTGCCCGCGCACCCGAAACCGGGGGA 12099
QY 901 ACTTCAGGTCCTTGGCATGCGCGTCTCCCATATCACTCGGACGGGATGGAAGCACACCG 960
Db |||||
12100 ACTTCAGGTCCTTGGCATGCGCGTCTCCCATATCACTCGGACGGGATGGAAGCACACCG 12159
QY 961 TCGTCTTGGGGTGC CGGTTCAGGAATGCGACTGTTGCTTGTAGTTTCAAGCGATCGATCC 1020
Db |||||
12160 TCGTCTTGGGGTGC CGGTTCAGGAATGCGACTGTTGCTTGTAGTTTCAAGCGATCGATCC 12219
QY 1021 AGTAGTCGTCCGCTCGCACACGCGACGTACTCGCGCGAGCGGCGGACAGGCGCGCG 1080
Db |||||
12220 AGTAGTCGTCCGCTCGCACACGCGACGTACTCGCGCGAGCGGCGGACAGGCGCGCG 12279
QY 1081 TCAGGTTCCATTTGAGCCGAGGTTTTCGTCTCTGAAGATCGCCGGAACAGTTCGCGGT 1140
Db |||||
12280 TCAGGTTCCATTTGAGCCGAGGTTTTCGTCTCTGAAGATCGCCGGAACAGTTCGCGGT 12339
QY 1141 ACCGCTCGGCGTACTCACGGATGATCGCGGGGTGGCATCGGTTCGACGCGTCTGCGGCA 1200
Db |||||
12340 ACCGCTCGGCGTACTCACGGATGATCGCGGGGTGGCATCGGTTCGACGCGTCTGCGGCA 12399
QY 1201 CGATGATCTCCACCGGGAGTTCGTTGCTGCTCGAGAAAGCTGTCGAAGGCTGACCGG 1260
Db |||||
12400 CGATGATCTCCACCGGGAGTTCGTTGCTGCTCGAGAAAGCTGTCGAAGGCTGACCGG 12459
QY 1261 CGTAGCCGCTGTTGTGAGTGTGAGACGATGCTCACTTGGGGCAAAAGCTGGGAC 1320
Db |||||
12460 CGTAGCCGCTGTTGTGAGTGTGAGACGATGCTCACTTGGGGCAAAAGCTGGGAC 12519
QY 1321 TCACGCTCGGCGCTTTTCTGCGCGCGCCGCAAGGGTATTGCGATGCGCAACGTGAATCG 1380
Db |||||
12520 TCACGCTCGGCGCTTTTCTGCGCGCGCCGCAAGGGTATTGCGATGCGCAACGTGAATCG 12579
QY 1381 CTGTGCGCGCGCGCTGCGCGCTGTTGCGTGGTTCGCGGAGCTACGGCACACGCT 1440

Db 12580 CTGTGCGCGCGCGCTGCGCGCTGTTGCGCTGTTGCGGAGCTACGGCACACGCT 12639
QY 1441 GCCGAAGTATACGAGGGTGCACTGACGTTGGGCTCGAAACCGCGTGGCGCGGTTGGG 1500
Db 12640 GCCGAAGTATACGAGGGTGCACTGACGTTGGGCTCGAAACCGCGTGGCGCGGTTGGG 12699
QY 1501 CCACCGCTTCAGTTCGGTCTGGTTCGCTCC 1533
Db 12700 CCACCGCTTCAGTTCGGTCTGGTTCGCTCC 12732

RESULT 2
US-09-670-314-1
; Sequence 1, Application US/09670314
; Patent No. 6492506
; GENERAL INFORMATION:
; APPLICANT: Cole, Stewart
; APPLICANT: Buchrieser-Brosch, Roland
; APPLICANT: Gordon, Stephen
; APPLICANT: Billault, Alain
; TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM
; TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA
; TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA
; FILE REFERENCE: 3495-0169
; CURRENT APPLICATION NUMBER: US/09/670,314
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/060,756
; PRIOR FILING DATE: 1998-04-16
; NUMBER OF SEQ ID NOS: 743
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 12732
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-09-670-314-1

Query Match 100.0%; Score 1533; DB 3; Length 12732;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1533; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTTTCAGTCCGGAACCTCGATCCCGAGGACCTGAAATCCCATCGCGCGGAACCCGACC 60
Db |||||
11200 ATGTTTCAGTCCGGAACCTCGATCCCGAGGACCTGAAATCCCATCGCGCGGAACCCGACC 11259
QY 61 GGTACCCGCTTCCAAGCAGCCGACATCGGCGAGCGTAGGTGGCTCTTGTCCCGGGA 120
Db |||||
11260 GGTACCCGCTTCCAAGCAGCCGACATCGGCGAGCGTAGGTGGCTCTTGTCCCGGGA 11319
QY 121 AAGACGGTTTCAGAAATCCCGCGCGGAGATGAACCCAGGACGATTCGTCATCGTCGC 180
Db |||||
11320 AAGACGGTTTCAGAAATCCCGCGCGGAGATGAACCCAGGACGATTCGTCATCGTCGC 11379
QY 181 GAGGACTCCGGTATCGTCAAGGTTCCGTGTCATCACTTGTAGCCCTTTCGGCTGCTCTGG 240
Db |||||
11380 GAGGACTCCGGTATCGTCAAGGTTCCGTGTCATCACTTGTAGCCCTTTCGGCTGCTCTGG 11439
QY 241 ACCGCGCGCGCGGAAATGTTCTGTCATCACTTGTAGCCCTTTCGGCTGCTCTGG 300
Db |||||
11440 ACCGCGCGCGCGGAAATGTTCTGTCATCACTTGTAGCCCTTTCGGCTGCTCTGG 11499
QY 301 TTTGTGCAATGGTCAGGCTCGACAGCGCGTTCGAGCGCGGAGGCGCACATCCACGA 360
Db |||||
11500 TTTGTGCAATGGTCAGGCTCGACAGCGCGTTCGAGCGCGGAGGCGCACATCCACGA 11559
QY 361 GCCCCTCGGCTCGGCGTTCGCGCGGAGCTTCGCCACTTGGCTTGGCTTGGCTTGGCTTGG 420
Db |||||
11560 GCCCCTCGGCTCGGCGTTCGCGCGGAGCTTCGCCACTTGGCTTGGCTTGGCTTGGCTTGG 11619
QY 421 CGGGTGTGCCCGCGGCTGCTCAGCGCGCAGCATGCGGATCCGGGATCGCGCGCATGG 480
Db |||||
11620 CGGGTGTGCCCGCGGCTGCTCAGCGCGCAGCATGCGGATCCGGGATCGCGCGCATGG 11679

Qy	481	TTTTCTGTGACGGCGCGCCCTCTCGGCGCCTTGGAACGTTGGCGATCTGGCGAAGGATCC	540
Db	11680	TTTTCTGTGACGGCGCGCGCCCTCTCGGCGCCTTGGAACGTTGGCGATCTGGCGAAGGATCC	11739
Qy	541	AGTCGGGCATGACCGGGCGATGAGCTCTCTCGCGCGCGGGTCTCCCGGGAAACAGGTCAGCA	600
Db	11740	AGTCGGGCATGACCGGCATGAGCTCTCTCGCGCGCGGGTCTCCCGGGAACAGGTCAGCA	11799
Qy	601	TCGGGTCAAAAGTCGCGGCATGCCCCGGHACCTTGCGTCAACAGAACTTTTGGCGGGTCA	660
Db	11800	TCGGGTCAAAAGTCGCGGCATGCCCCGGHACCTTGCGTCAACAGAACTTTTGGCGGGTCA	11859
Qy	661	CCACCTGGTTGTGCCACATGCTTTGGCGCTGGCGGCGATACACGGCCATGGTGTCTGGCA	720
Db	11860	CCACCTGGTTGTGCCACATGCTTTGGCGCTGGCGGCGATACACGGCCATGGTGTCTGGCA	11919
Qy	721	ACATGGCGATGTCCGCATGACCGCGTGCGGACGFTGCAGATACACAGTCCAGGGGCATGA	780
Db	11920	ACATGGCGATGTCCGCATGACCGCGTGCGGACGFTGCAGATACACAGTCCAGGGGCATGA	11979
Qy	781	CGTCGCGAGAAATGTCGTGCTAGCGCTCCAGCGACGGTACACGCCGAGTTGTCGTA	840
Db	11980	CGTCGCGAGAAATGTCGTGCTAGCGCTCCAGCGACGGTACACGCCGAGTTGTCGTA	12039
Qy	841	TGAAGTTTCATCAAGATCAACGCATCCAGGCTCAAGTTTGCCCGCGCACCCGAAACCGGGGGA	900
Db	12040	TGAAGTTTCATCAAGATCAACGCATCCAGGCTCAAGTTTGCCCGCGCACCCGAAACCGGGGGA	12099
Qy	901	ACTTCGAGTCTTTGGCATGCGCGTCTCTCCCATATCACTCGHACGGGATGGAAGCAACCG	960
Db	12100	ACTTCGAGTCTTTGGCATGCGCGTCTCTCCCATATCACTCGHACGGGATGGAAGCAACCG	12159
Qy	961	TCGTCCTTGGGGTCCCGGTCGAGGAATGCGACCTGTTGCTTAGCTTCAGCGGATCGATCC	1020
Db	12160	TCGTCCTTGGGGTCCCGGTCGAGGAATGCGACCTGTTGCTTAGCTTCAGCGGATCGATCC	12219
Qy	1021	AGTAGTGTCTCCGCTTCGCAACAACGCGACGTATCTCGCCGCGAGCGCCGACAGGCGCCGG	1080
Db	12220	AGTAGTGTCTCCGCTTCGCAACAACGCGACGTATCTCGCCGCGAGCGCGCCGACAGGCGCCGG	12279
Qy	1081	TCAGGTTCCCATGAGGCGGAGGTTTTTCGGTCTTGAGATCGGCGGGHACACGTCGGGT	1140
Db	12280	TCAGGTTCCCATGAGGCGGAGGTTTTTCGGTCTTGAGATCGGCGGGHACACGTCGGGT	12339
Qy	1141	ACCGCTCGGCGTACTCACGCGATGATCGCGGGGTGGCATCGGTGCAACGCGTCTCGCGCA	1200
Db	12340	ACCGCTCGGCGTACTCACGCGATGATCGCGGGGTGGCATCGGTGCAACGCGTCTCGCGCA	12399
Qy	1201	CGATGATCTTCACCGGGAAAGTCGGTTGTGFTCGAGAAAGCTGTGCAAGGCTTGACGGG	1260
Db	12400	CGATGATCTTCACCGGGAAAGTCGGTTGTGFTCGAGAAAGCTGTGCAAGGCTTGACGGG	12459
Qy	1261	CGTAGCCGCGCTGGTTGTGAGTGTGTCGACACGATGCTACCTTTGGGCAAAAGCTGGGGAC	1320
Db	12460	CGTAGCCGCGCTGGTTGTGAGTGTGTCGACACGATGCTACCTTTGGGCAAAAGCTGGGGAC	12519
Qy	1321	TCACCGTCGGCCCTTTTCTTCGCGCGCCGCAAGGGTATTTGCGATGCGCAACGTGAATCGC	1380
Db	12520	TCACCGTCGGCCCTTTTCTTCGCGCGCCGCAAGGGTATTTGCGATGCGCAACGTGAATCGC	12579
Qy	1381	CTGTGCCCGCGCGCTCGGCGCTCGTGGCGCTTGGTGGTGGGACGTACGGCAACGCT	1440
Db	12580	CTGTGCCCGCGCGCTCGGCGCTCGTGGCGCTTGGTGGTGGGACGTACGGCAACGCT	12639
Qy	1441	GGCGAAGTATAGCGAGGCTGCACTGACGTTTGGGCTCGAAGCCGCTGGCGCGCGGTGGG	1500
Db	12640	GGCGAAGTATAGCGAGGCTGCACTGACGTTTGGGCTCGAAGCCGCTGGCGCGCGGTGGG	12699
Qy	1501	CGCACCGTCTCGAGTCGGTGTGGTGGTGTGCTCGC	1533
Db	12700	CGCACCGTCTCGAGTCGGTGTGGTGGTGTGCTCGC	12732

RESULT 3
US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24 *
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

2

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QY 661 CCACCTGGTGTGGCCATGCTTGGCGTGGGGGATACACGGCCATGGTGTGGGGCA 720
Db 1708003 CCACCTGGTGTGGCCATGCTTGGCGTGGGGGATACACGGCCATGGTGTGGGGCA 1708062
QY 721 ACATGCGGATGTGCGCATCACCGGTGCGGACGTGCAGATACCAAGTCCAGGGGCATGA 780
Db 1708063 ACATGCGGATGTGCGCATCACCGGTGCGGACGTGCAGATACCAAGTCCAGGGGCATGA 1708122
QY 781 CGTCGGCAGGAATGTGCTGATAGCGTTCGAGCGCAGCGGTACACGGCCGAGTTGGTCTGGA 840
Db 1708123 CGTCGGCAGGAATGTGCTGATAGCGTTCGAGCGCAGCGGTACACGGCCGAGTTGGTCTGGA 1708182
QY 841 TGAAGTTTCATCAAGATCAACGATCAGAGCTCAAGTTCGCCCGCCGACCCCGAACCAGGGGGGA 900
Db 1708183 TGAAGTTTCATCAAGATCAACGATCAGAGCTCAAGTTCGCCCGCCGACCCCGAACCAGGGGGGA 1708242
QY 901 ACTTCGAGTCTTGGCATCGCGCTCTCCATATCACTCGGACGGGATGGAAGCACACCG 960
Db 1708243 ACTTCGAGTCTTGGCATCGCGCTCTCCATATCACTCGGACGGGATGGAAGCACACCG 1708302
QY 961 TCGTCTTGGGGTGC CGGTTCAGGAAATGCGACCTGTTGCTTAGCTTCAGCGGATCGATCC 1020
Db 1708303 TCGTCTTGGGGTGC CGGTTCAGGAAATGCGACCTGTTGCTTAGCTTCAGCGGATCGATCC 1708362
QY 1021 AGTAGTCGTCGCGCTCGCAACAGCGACGTACTCGCGCGAGGCGCGACAGGGCGCGG 1080
Db 1708363 AGTAGTCGTCGCGCTCGCAACAGCGACGTACTCGCGCGAGGCGCGACAGGGCGCGG 1708422
QY 1081 TCAGGTTCCATGAGCGCGAGGTTTTCGCTCTGAAGATCGGCGGACACAGTGGCGGT 1140
Db 1708423 TCAGGTTCCATGAGCGCGAGGTTTTCGCTCTGAAGATCGGCGGACACAGTGGCGGT 1708482
QY 1141 ACCGCTCGGCGTACTCACGGATGATCGCGCGGGTGGCATCGGTTCGACGCGTCTGCGGCA 1200
Db 1708483 ACCGCTCGGCGTACTCACGGATGATCGCGCGGGTGGCATCGGTTCGACGCGTCTGCGGCA 1708542
QY 1201 CGATGATCTCCACCGGGAAGTCGTTGCTGTGTCGAGAAAGCTGTGCAAGGCGTGCAGGG 1260
Db 1708543 CGATGATCTCCACCGGGAAGTCGTTGCTGTGTCGAGAAAGCTGTGCAAGGCGTGCAGGG 1708602
QY 1261 CGTAGCGCGCTGTTGTCAAGTGTGCGACAGATGCTCACCTTGGGGCAAAAGCTGGGGAC 1320
Db 1708603 CGTAGCGCGCTGTTGTGAGTGTGTCGACAGATGCTCACCTTGGGGCAAAAGCTGGGGAC 1708662
QY 1321 TCACCGTTCGCGCGCTTTTCTGCGCGGCGCAAGGGTATTGCGATGGCGAAACGTGAATCGC 1380
Db 1708663 TCACCGTTCGCGCGCTTTTCTGCGCGGCGCAAGGGTATTGCGATGGCGAAACGTGAATCGC 1708722
QY 1381 CTGTGCGCGCGCGCGTCTGCGCGCGTCTGTCGCGTGGTGTGTCGCGGACGTAACGCT 1440
Db 1708723 CTGTGCGCGCGCGCGTCTGCGCGCGTCTGTCGCGTGGTGTGTCGCGGACGTAACGCT 1708782
QY 1441 GCGGAAGTATAGCAGGGTGCACTGACGTTGGCTCGAAACCGCTGGCGCGCGTGTGGG 1500
Db 1708783 GCGGAAGTATAGCAGGGTGCACTGACGTTGGCTCGAAACCGCTGGCGCGCGTGTGGG 1708842
QY 1501 CGCACCGTCTCGAGTCGGTGTGCTGGTGGCTCGC 1533
Db 1708843 CGCACCGTCTCGAGTCGGTGTGCTGGTGGCTCGC 1708875
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RESULT 4

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US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
```

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; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1
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Query Match 100.0%; Score 1533; DB 3; Length 4411529;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1533; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTTTCAGTCTCGGAACCTTCGATCCCGAGGACCTTGAAATCCCATGCGCGCAACCCGACC 60
Db 1707214 ATGTTTCAGTCTCGGAACCTTCGATCCCGAGGACCTTGAAATCCCATGCGCGCAACCCGACC 1707273
QY 61 GCGTACCGCGCTTCCAAAGCAGCGGACATCGGCGAGCGGTAGGTGGCTCTTTGTCCCGCGGA 120
Db 1707274 GCGTACCGCGCTTCCAAAGCAGCGGACATCGGCGAGCGGTAGGTGGCTCTTTGTCCCGCGGA 1707333
QY 121 AAGACGCTTTCAGAAATCCCGCGCGGAGATGAACAGGACGATTCGCTTAACGTGCGC 180
Db 1707334 AAGACGCTTTCAGAAATCCCGCGCGGAGATGAACAGGACGATTCGCTTAACGTGCGC 1707393
QY 181 GAGGACTCCGGTATCGTCAAGGTTCCGTCGTGAGCGCGAAGCGTTGTGGCGGTGAATTGT 240
Db 1707394 GAGGACTCCGGTATCGTCAAGGTTCCGTCGTGAGCGCGAAGCGTTGTGGCGGTGAATTGT 1707453
QY 241 ACCGCGCGCGCGAAGTTTCCTGTGTCATCACTTGGTTAGACCCCTTTCGCGTGGTCTCGG 300
Db 1707454 ACCGCGCGCGCGAAGTTTCCTGTGTCATCACTTGGTTAGACCCCTTTCGCGTGGTCTCGG 1707513
QY 301 TTTGTGCAATGTCAGGCTCGACAGCGCGCTCGAGCGCGGAGCGGAGGCGCACATCCACGA 360
Db 1707514 TTTGTGCAATGTCAGGCTCGACAGCGCGCTCGAGCGCGGAGGCGCACATCCACGA 1707573
QY 361 GCGCGCTCGCGCTCGCGCGTTCGCGCGGCGGAGCTTTCGCGCACTTGGTCTTTCGAGCGCGCG 420
Db 1707574 GCGCGCTCGCGCTCGCGCGTTCGCGCGGCGGAGCTTTCGCGCACTTGGTCTTTCGAGCGCGCG 1707633
QY 421 CGGGTGTCCCGCGGTGCTGCGCGCGCAGCATGCGCGATGCGCGGATGCGCGCGATGG 480
Db 1707634 CGGGTGTCCCGCGGTGCTGCGCGCGCAGCATGCGCGATGCGCGGATGCGCGCGATGG 1707693
QY 481 TTTTCCTGCAAGCGCGCGCGCGCTTCGCGCGCTGGAACGTTGGCGATCTCGCGAAGGATCC 540
Db 1707694 TTTTCCTGCAAGCGCGCGCGCGCTTCGCGCGCTGGAACGTTGGCGATCTCGCGAAGGATCC 1707753
QY 541 AGTCGCGCATGACGCGCGATGAGCTCTCTCGCGCGCGGGGTCTCCCGGGAAACAGGTTCGAGCA 600
Db 1707754 AGTCGCGCATGACGCGCGATGAGCTCTCTCGCGCGCGGGGTCTCCCGGGAAACAGGTTCGAGCA 1707813
QY 601 TCGGTCAAAAGTCGCGCATGCGCGGACCCCGGACCCCTGTGTCGTCGTCGTCGTCGTCGTCG 660
Db 1707814 TCGGTCAAAAGTCGCGCATGCGCGGACCCCGGACCCCTGTGTCGTCGTCGTCGTCGTCGTCG 1707873
QY 661 CCACCTGGTGTGCGACATGCTTGGCGGTGGCGGATACACGGCGATGCTGTCGCGGCA 720
Db 1707874 CCACCTGGTGTGCGACATGCTTGGCGGTGGCGGATACACGGCGATGCTGTCGCGGCA 1707933
QY 721 ACATGGCGATGTGCGCATGCGCGGTGCGCGGACGTGCGAGATACCAAGTCCAGGGGCATGA 780
Db 1707934 ACATGGCGATGTGCGCATGCGCGGTGCGCGGACGTGCGAGATACCAAGTCCAGGGGCATGA 1707993
QY 781 CGTCGCGAGGAATGTGCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 840
Db 1707994 CGTCGCGAGGAATGTGCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1708053
QY 841 TGAAGTTTCATCAAGATCAACGATCCAGGCTCAAGTTGCCCCCGCCGACCCCGAACCAGGGGGGA 900
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[illegible]

RESULT 5

US-09-894-844-53/c					
; Sequence 53, Application US/09894844					
; Patent No. 6686166					
; GENERAL INFORMATION:					
; APPLICANT: Behr, Marcel					
; APPLICANT: Small, Peter					
; APPLICANT: Schoolnik, Gary					
; APPLICANT: Wilson, Michael A.					
; TITLE OF INVENTION: Molecular Differences Between Species of					
; TITLE OF INVENTION: the M. Tuberculosis Complex					
; FILE REFERENCE: STAN102CON					
; CURRENT APPLICATION NUMBER: US/09/894,844					
; CURRENT FILING DATE: 2001-06-27					
; PRIOR APPLICATION NUMBER: 09/318,191					
; PRIOR FILING DATE: 1999-05-25					
; PRIOR APPLICATION NUMBER: 60/097,936					
; PRIOR FILING DATE: 1998-08-25					
; NUMBER OF SEQ ID NOS: 137					
; SOFTWARE: FastSeq for Windows Version 4.0					
; SEQ ID NO 53					
; LENGTH: 1119					
; TYPE: DNA					
; ORGANISM: Mycobacteria tuberculosis					
US-09-894-844-53					

QY	977	GTGAGGAATCGGACCTGTTTGCTTAGCTTCAGCCGATCGATCCAGTAGTGGTCCGCCTC	1036
DB	459	GTGAGGAATCGGACCTGTTTGCTTAGCTTCAGCCGATCGATCCAGTAGTGGTCCGCCTC	400
QY	1037	GCACAAACGCCACTACTCGCCGAGCGCGCACAGGGCCCGGTACAGTTCCTCATTTGAG	1096
DB	399	GCACAAACGCCACTACTCGCCGAGCGCGCACAGGGCCCGGTACAGTTCCTCATTTGAG	340
QY	1097	GCCGAGGTTTTCGGTCTCTGAAGATCGCCCGGAAACAAGTGGGGTACCGTTCGCGGTACTC	1156
DB	339	GCCGAGGTTTTCGGTCTCTGAAGATCGCCCGGAAACAAGTGGGGTACCGTTCGCGGTACTC	280
QY	1157	ACGGATGATCGCGGGGTGGCATCGGTCTGTCGGCGGACGATGATCTCCACCGG	1216
DB	279	ACGGATGATCGCGGGGTGGCATCGGTCTGTCGGCGGACGATGATCTCCACCGG	220
QY	1217	GAAAGTCGGTTTTGCTGTCGAGAAAAGCTGTGCAAGGCCTGACGGGCGGTAGCCCCCTGGTT	1276
DB	219	GAAAGTCGGTTTTGCTGTCGAGAAAAGCTGTGCAAGGCCTGACGGGCGGTAGCCCCCTGGTT	160
QY	1277	GTGAGTGTTCGAGACGATGCTCACTTTGGGGCAAGCTGGGGACTACCCTCGGCCCTTT	1336
DB	159	GTGAGTGTTCGAGACGATGCTCACTTTGGGGCAAGCTGGGGACTACCCTCGGCCCTTT	100

QY 712 TGTGGGCAACATGGCGATGTCGCAATGACCCGCTGCGGAGCTGCAGATACCACTCCA 771
|
Db 1711611 TCTCGGGCAACATGGCGATGTCGCGCCACCCGATGCCCAATGCAAGTACCAATCTA 1711552
|
QY 772 GGGGCAATGACGTCGGCAGGAATGTCGTGAGCGCTCGAGGCGACGGTACACGCGCGAGT 831
|
Db 1711551 TCGGCATGACGTTGGCGGGGATGTCGTGAGTCTCGGTCGACGGCGGTACACGACCGAGT 1711492
|
QY 832 TGGTCTGGATGAGTTTCATCAAGATCAACGATCCAGCTCAGGCTCAAGTTGCCCGCACCCGAA 891
|
Db 1711491 TGGTTGGATGAAATTCGCGCGAGCAGGCGCATCGACGCTCAGGTCGCGCGCGCACTGA 1711432
|
QY 892 CCGGGGGAACTTCGAGTCTTGGCATGCGCGTCCCTCCCATATCACTCGAGCGGGATGGA 951
|
Db 1711431 GCGGGGGAACTCGGAGTCTTTTGC---GCCATCTCATAGATCACTCGCACAGATGAA 1711375
|
QY 952 AGCACACCGTGTCTTGGGGTGGCGGTGCGGAGGAATCGACCTGTTTGTAGCTTCAGCG 1011
|
Db 1711374 AACACACCGTGTCTCGGATGCGGTCCAGGTACTTTACCTGTTGGACAGCTTCAGCG 1711315
|
QY 1012 GATCGATCCAGTAGTGTCTCGGCTCGCACACCGGAGTACTCGCGCGAGCGGCGGACA 1071
|
Db 1711314 GATCGTCCAGTAATCGTCCGCTTCGCACAGTCGAGGTACTCGCCACGAGCGCGGACA 1711255
|
QY 1072 GGGCGCGGTGAGTTCCCATTCAGGCGCGAGGTTTTCGGTCTTGAAGATCGGCGGGAACA 1131
|
Db 1711254 GCATCTCTTGAATTTGGGTGAGACCGATGTTGGTCTGCCCGAGATCGGCGGAACA 1711195
|
QY 1132 CGTGGGTGACCGTCTCGGCTACTCACGATGATCGCGGGTGGCATCGGTGCGAGCGT 1191
|
Db 1711194 GCTGGGATAGCGGGCGGTACTCTCTATGATCTCGGGTGGGTCTCGTGGAGCAT 1711135
|
QY 1192 CGTGGCGAGCATGATCTCACCGGAAGTGTGTTGCTGCTGAGGAAAGCTGTGCAAGG 1251
|
Db 1711134 CGTCAGCATGATCACTCGACGGGAACTCGGTCTCTGCGGCGGGAAGCGTCCAGG 1711075
|
QY 1252 CTTGACGGGTAGCGCGCTGCTGTGAGTGTGCGAGCATGCTCACTTGGGGCAA 1310
|
Db 1711074 CTTGCGAATGACTCTCTTGGTTGTAGAGATCGAGAGTACTCACTTGGGCGAA 1711016
|

RESULT 8

US-09-894-844-52/c

; Sequence 52, Application US/09894844

; Patent No. 6686166

; GENERAL INFORMATION:

; APPLICANT: Behr, Marcel

; APPLICANT: Small, Peter

; APPLICANT: Schoolnik, Gary

; APPLICANT: Wilson, Michael A.

; TITLE OF INVENTION: Molecular Differences Between Species of

; FILE REFERENCE: the M. Tuberculosis Complex

; CURRENT APPLICATION NUMBER: US/09/894,844

; CURRENT FILING DATE: 2001-06-27

; PRIOR APPLICATION NUMBER: 09/318,191

; PRIOR FILING DATE: 1999-05-25

; PRIOR APPLICATION NUMBER: 60/097,936

; PRIOR FILING DATE: 1998-08-25

; NUMBER OF SEQ ID NOS: 137

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 52

; LENGTH: 894

; TYPE: DNA

; ORGANISM: Mycobacteria tuberculosis

US-09-894-844-52

Query Match

Best Local Similarity 20.3%; Score 311; DB 3; Length 894;

; Sequence 52, Application US/09894844

; Patent No. 6686166

; GENERAL INFORMATION:

; APPLICANT: Behr, Marcel

; APPLICANT: Small, Peter

; APPLICANT: Schoolnik, Gary

; APPLICANT: Wilson, Michael A.

; TITLE OF INVENTION: Molecular Differences Between Species of

; FILE REFERENCE: the M. Tuberculosis Complex

; CURRENT APPLICATION NUMBER: US/09/894,844

; CURRENT FILING DATE: 2001-06-27

; PRIOR APPLICATION NUMBER: 09/318,191

; PRIOR FILING DATE: 1999-05-25

; PRIOR APPLICATION NUMBER: 60/097,936

; PRIOR FILING DATE: 1998-08-25

; NUMBER OF SEQ ID NOS: 137

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 52

; LENGTH: 894

; TYPE: DNA

; ORGANISM: Mycobacteria tuberculosis

US-09-894-844-52

Query Match

Best Local Similarity 100.0%; Score 311; DB 3; Length 894;

; Sequence 52, Application US/09894844

; Patent No. 6686166

; GENERAL INFORMATION:

; APPLICANT: Behr, Marcel

; APPLICANT: Small, Peter

; APPLICANT: Schoolnik, Gary

; APPLICANT: Wilson, Michael A.

; TITLE OF INVENTION: Molecular Differences Between Species of

; FILE REFERENCE: the M. Tuberculosis Complex

; CURRENT APPLICATION NUMBER: US/09/894,844

; CURRENT FILING DATE: 2001-06-27

; PRIOR APPLICATION NUMBER: 09/318,191

; PRIOR FILING DATE: 1999-05-25

; PRIOR APPLICATION NUMBER: 60/097,936

; PRIOR FILING DATE: 1998-08-25

; NUMBER OF SEQ ID NOS: 137

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 52

; LENGTH: 894

; TYPE: DNA

; ORGANISM: Mycobacteria tuberculosis

US-09-894-844-52

Query Match

Best Local Similarity 100.0%; Score 311; DB 3; Length 894;

; Sequence 52, Application US/09894844

; Patent No. 6686166

; GENERAL INFORMATION:

; APPLICANT: Behr, Marcel

; APPLICANT: Small, Peter

; APPLICANT: Schoolnik, Gary

; APPLICANT: Wilson, Michael A.

; TITLE OF INVENTION: Molecular Differences Between Species of

; FILE REFERENCE: the M. Tuberculosis Complex

; CURRENT APPLICATION NUMBER: US/09/894,844

; CURRENT FILING DATE: 2001-06-27

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; PRIOR FILING DATE: 1999-05-25

; PRIOR APPLICATION NUMBER: 60/097,936

; PRIOR FILING DATE: 1998-08-25

; NUMBER OF SEQ ID NOS: 137

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 52

; LENGTH: 894

; TYPE: DNA

; ORGANISM: Mycobacteria tuberculosis

US-09-894-844-52

Query Match

Best Local Similarity 100.0%; Score 311; DB 3; Length 894;

; Sequence 52, Application US/09894844

; Patent No. 6686166

; GENERAL INFORMATION:

; APPLICANT: Behr, Marcel

; APPLICANT: Small, Peter

; APPLICANT: Schoolnik, Gary

; APPLICANT: Wilson, Michael A.

; TITLE OF INVENTION: Molecular Differences Between Species of

; FILE REFERENCE: the M. Tuberculosis Complex

; CURRENT APPLICATION NUMBER: US/09/894,844

; CURRENT FILING DATE: 2001-06-27

; PRIOR APPLICATION NUMBER: 09/318,191

; PRIOR FILING DATE: 1999-05-25

; PRIOR APPLICATION NUMBER: 60/097,936

; PRIOR FILING DATE: 1998-08-25

; NUMBER OF SEQ ID NOS: 137

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 52

; LENGTH: 894

; TYPE: DNA

; ORGANISM: Mycobacteria tuberculosis

US-09-894-844-52

Query Match

Best Local Similarity 100.0%; Score 311; DB 3; Length 894;

; Sequence 52, Application US/09894844

; Patent No. 6686166

; GENERAL INFORMATION:

; APPLICANT: Behr, Marcel

; APPLICANT: Small, Peter

; APPLICANT: Schoolnik, Gary

; APPLICANT: Wilson, Michael A.

; TITLE OF INVENTION: Molecular Differences Between Species of

; FILE REFERENCE: the M. Tuberculosis Complex

; CURRENT APPLICATION NUMBER: US/09/894,844

; CURRENT FILING DATE: 2001-06-27

; PRIOR APPLICATION NUMBER: 09/318,191

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; PRIOR APPLICATION NUMBER: 60/097,936

; PRIOR FILING DATE: 1998-08-25

; NUMBER OF SEQ ID NOS: 137

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 52

; LENGTH: 894

; TYPE: DNA

; ORGANISM: Mycobacteria tuberculosis

US-09-894-844-52

Query Match

Best Local Similarity 100.0%; Score 311; DB 3; Length 894;

; Sequence 52, Application US/09894844

; Patent No. 6686166

; GENERAL INFORMATION:

; APPLICANT: Behr, Marcel

; APPLICANT: Small, Peter

; APPLICANT: Schoolnik, Gary

; APPLICANT: Wilson, Michael A.

; TITLE OF INVENTION: Molecular Differences Between Species of

; FILE REFERENCE: the M. Tuberculosis Complex

; CURRENT APPLICATION NUMBER: US/09/894,844

; CURRENT FILING DATE: 2001-06-27

; PRIOR APPLICATION NUMBER: 09/318,191

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; PRIOR APPLICATION NUMBER: 60/097,936

; PRIOR FILING DATE: 1998-08-25

; NUMBER OF SEQ ID NOS: 137

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 52

; LENGTH: 894

; TYPE: DNA

; ORGANISM: Mycobacteria tuberculosis

US-09-894-844-52

Query Match

Best Local Similarity 100.0%; Score 311; DB 3; Length 894;

; Sequence 52, Application US/09894844

; Patent No. 6686166

; GENERAL INFORMATION:

; APPLICANT: Behr, Marcel

; APPLICANT: Small, Peter

; APPLICANT: Schoolnik, Gary

; APPLICANT: Wilson, Michael A.

; TITLE OF INVENTION: Molecular Differences Between Species of

; FILE REFERENCE: the M. Tuberculosis Complex

; CURRENT APPLICATION NUMBER: US/09/894,844

; CURRENT FILING DATE: 2001-06-27

; PRIOR APPLICATION NUMBER: 09/318,191

; PRIOR FILING DATE: 1999-05-25

; PRIOR APPLICATION NUMBER: 60/097,936

; PRIOR FILING DATE: 1998-08-25

; NUMBER OF SEQ ID NOS: 137

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 52

; LENGTH: 894

; TYPE: DNA

; ORGANISM: Mycobacteria tuberculosis

US-09-894-844-52

Query Match

Best Local Similarity 100.0%; Score 311; DB 3; Length 894;

; Sequence 52, Application US/09894844

; Patent No. 6686166

; GENERAL INFORMATION:

; APPLICANT: Behr, Marcel

; APPLICANT: Small, Peter

; APPLICANT: Schoolnik, Gary

; APPLICANT: Wilson, Michael A.

; TITLE OF INVENTION: Molecular Differences Between Species of

; FILE REFERENCE: the M. Tuberculosis Complex

; CURRENT APPLICATION NUMBER: US/09/894,844

; CURRENT FILING DATE: 2001-06-27

; PRIOR APPLICATION NUMBER: 09/318,191

; PRIOR FILING DATE: 1999-05-25

; PRIOR APPLICATION NUMBER: 60/097,936

; PRIOR FILING DATE: 1998-08-25

; NUMBER OF SEQ ID NOS: 137

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 52

; LENGTH: 894

; TYPE: DNA

; ORGANISM: Mycobacteria tuberculosis

US-09-894-844-52

Query Match

Best Local Similarity 100.0%; Score 311; DB 3; Length 894;

; Sequence 52, Application US/09894844

; Patent No. 6686166

; GENERAL INFORMATION:

; APPLICANT: Behr, Marcel

; APPLICANT: Small, Peter

; APPLICANT: Schoolnik, Gary

; APPLICANT: Wilson, Michael A.

; TITLE OF INVENTION: Molecular Differences Between Species of

; FILE REFERENCE: the M. Tuberculosis Complex

; CURRENT APPLICATION NUMBER: US/09/894,844

; CURRENT FILING DATE: 2001-06-27

; PRIOR APPLICATION NUMBER: 09/318,191

; PRIOR FILING DATE: 1999-05-25

; PRIOR APPLICATION NUMBER: 60/097,936

; PRIOR FILING DATE: 1998-08-25

; NUMBER OF SEQ ID NOS: 137

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 52

; LENGTH: 894

; TYPE: DNA

; ORGANISM: Mycobacteria tuberculosis

US-09-894-844-52

Query Match

Best Local Similarity 100.0%; Score 311; DB 3; Length 894;

; Sequence 52, Application US/09894844

; Patent No. 6686166

; GENERAL INFORMATION:

; APPLICANT: Behr, Marcel

; APPLICANT: Small, Peter

; APPLICANT: Schoolnik, Gary

; APPLICANT: Wilson, Michael A.

; TITLE OF INVENTION: Molecular Differences Between Species of

; FILE REFERENCE: the M. Tuberculosis Complex

; CURRENT APPLICATION NUMBER: US/09/894,844

; CURRENT FILING DATE: 2001-06-27

; PRIOR APPLICATION NUMBER: 09/318,191

; PRIOR FILING DATE: 1999-05-25

; PRIOR APPLICATION NUMBER: 60/097,936

; PRIOR FILING DATE: 1998-08-25

; NUMBER OF SEQ ID NOS: 137

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 52

; LENGTH: 894

; TYPE: DNA

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; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 2466
; LENGTH: 1574
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-540-2466

Query Match          3.7%; Score 56; DB 3; Length 1574;
Best Local Similarity 47.1%; Pred. No. 0.0052;
Matches 241; Conservative 0; Mismatches 265; Indels 6; Gaps 2;

QY 335 CCACGAGCCCCCTGCGGCTCGCGCTCGCGCGCGCGGAGCTTGGCCCACTGGGCTCTTGAGCC 414
DB 1224 CCACCACCGCTCTGCGCGCCCTTCATGTCGCGATGACCTGGGCGCACCTGG-----GCGGC 1170

QY 415 GCGCGCGGGTGTCTGCGCCCGCGGTCTGTCAGCGCCAGCATGCGATGCGGGGATGGCGG 474
DB 1169 GACGGCGGGATCAACCCGCGCGGTG-GGCTCGTCAGCAGCACCACGCGCGGGCTGCCCA 1111

QY 475 CGATGTTTCTTCGACGCGCGCGCCCTTCGCGGCTTGGAACGTTGGCGATCTGGCGAA 534
DB 1110 TGAGGCGCTTGGGCCATGGCGCGCGCTTGCCCATGCGGTGGCTGAGCGCTCTGTCTGGA 1051

QY 535 GATCAGTCGCGCATGACGCGGATGAGTCTCTCGCGCGCGGGTCTCCGCGGAACAGT 594
DB 1050 CGTTCCAGGCTCCATAGGCGCCACCTTGTCAGGCGCTTCGCGCGCTCACGCTCCGGCT 991

QY 595 CGAGCATCGCTCAACGTCGCGCGCATGCGCGGACCTTCGCTCAACAGAACTTTGGCG 654
DB 990 CGGCCAGGCGGACGCGCGCCAGTATCATAGCAGCGCGCCACTTCCGAGCGGGCG 931

QY 655 GTTCACCACTGGTTGTCACATGCTTGGCGCTGCGCGCGATACACGCGCATGGTGT 714
DB 930 GCAGCACCGGCTCTCGCGCAGCGCGCCGCGGCGCTTACGGGCGCGCGGGTGGTGG 871

QY 715 CCGGCAACATGCGGATGTCGATGCGCATGCGCGCTGCGGAGCTGCAGATACAGTCCAGG 774
DB 870 GGTCCACATCCATGACCTTTGAGCGAGCCCTTCGAGCGGGTAGAGGTAGCGCACATCATGG 811

QY 775 GCATGACGTCGCGAGGAATGTCGTAGCGCTCGAGGCGAGCTACGCGCGGAGTTGG 834
DB 810 AGAAGTGTCTCTTTCGCGCGCGCTTGGGCGCGATGAGCGCCGATGACCGCGCCCTTGG 751

QY 835 TCTGGATGAAGTTTCATCAAGATCAACGCGATCC 866
DB 750 GCACGAGAGCTGACCGCGTTGACGCGGACC 719

RESULT 11
US-09-902-540-1109
; Sequence 1109, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825

Query Match          3.5%; Score 54.4; DB 3; Length 9521;
Best Local Similarity 43.0%; Pred. No. 0.015;
Matches 433; Conservative 0; Mismatches 566; Indels 9; Gaps 3;

; SEQ ID NO 1109
; LENGTH: 14077
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-1109

Query Match          3.7%; Score 56; DB 3; Length 14077;
Best Local Similarity 47.1%; Pred. No. 0.0073;
Matches 241; Conservative 0; Mismatches 265; Indels 6; Gaps 2;

QY 355 CCACGAGCCCCCTGCGGCTCGCGCTCGCGCGCGCGGAGCTTGGCCCACTGGGCTCTTGAGCC 414
DB 6399 CCACCACCGCTCTGCGCGCCCTTCATGTCGCGATGACCTGGGCGCACCTGG-----GCGGC 6453

QY 415 GCGCGCGGGTGTCTGCGCCCGCGGTCTGTCAGCGCCAGCATGCGATGCGGGGATGGCGG 474
DB 6454 GACGCGCGGATCCAAACCCGCGCGGTG-GGCTCGTCAGCAGCACCACGCGCGGGCTGCCCA 6512

QY 475 CGATGTTTCTTCGACGCGCGCGCCCTTCGCGGCTTGGAACGTTGGCGATCTGGCGAA 534
DB 6513 TGAGGCGCTTGGGCCATGGCGCGCGCTTGCCCATGCGGTGGCTGAGCGCTCTGTCTGGA 6572

QY 535 GATCAGTCGCGCATGACGCGGATGAGTCTCTCGCGCGCGGGTCTCCGCGGAACAGT 594
DB 6573 CGTTCCAGGCTCCATGAGGCCACCTTGTCAGGCGCTTCGCGCGCTCACGCTCCGGCT 6632

QY 595 CGAGCATCGCTCAACGTCGCGCGCATGCGCGGACCTTCGCTCAACAGAACTTTGGCG 654
DB 6633 CGGCCAGGCGCGGACGCGCGCCAGTATCATGACGAGCGCGCCACTTCCGAGCGGGCG 6692

QY 655 GGTCCACCACTGGTTGTCACATGCTTGGCGCTTGGCGGCGATACACGCGCATGGTGT 714
DB 6693 GCAGCACCGCTCTTCGCGCAGCGCGCCAGCGCGCTTACGGGCGCGCGGGTGGTGG 6752

QY 715 CCGGCAACATGCGGATGTCGATGCGCATGCGCGCTGCGGAGCTGCAGATACAGTCCAGG 774
DB 6753 GGTCCACATCCATGACCTTTGAGCGAGCCCTTCGAGCGGGTAGAGGTAGCGCACATCATGG 6812

QY 775 GCATGACGTCGCGAGGAATGTCGTAGCGCTCGAGGCGAGCTACGCGCGGAGTTGG 834
DB 6813 AGAAGTGTCTCTTTCGCGCGCGCTTGGGCGCGATGAGCGCCGATGACCGCGCCCTTGG 6872

QY 835 TCTGGATGAAGTTTCATCAAGATCAACGCGATCC 866
DB 6873 GCACGAGAGCTGACCGCGTTGACGCGGACC 6904

RESULT 12
US-09-902-540-953
; Sequence 953, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 953
; LENGTH: 9521
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-953

Query Match          3.5%; Score 54.4; DB 3; Length 9521;
Best Local Similarity 43.0%; Pred. No. 0.015;
Matches 433; Conservative 0; Mismatches 566; Indels 9; Gaps 3;
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QY 66 CCGCGCTTCCAGAGCCGACATCGCCAGCGTAGTGCTCTTGTCCCGGAAAGAC 125
Db |||||
QY 5370 CTGCGCTCGACGACGAGGGTCGACGGGGCGCCCTCGGTGCTCTCCACCGGCCAGC 5429
Db |||||
QY 126 GGTTCAGAGATCCGCGCCGAGATGAACAGGACGATTCTTAACGTGCGCAGGA 185
Db |||||
QY 5430 GGTGGAAGCATGCTCTCGCGCTGCGGAGGCGCCCGGAGGGGACCCCGCGTGGCGGA 5489
Db |||||
QY 186 CTCCGGTATCGTCAAGGTTCCGTGCTGAGCGGAAAGTTGTGGCGGTGAATTGTACCGC 245
Db |||||
QY 5490 CTTGAGGGGATCGCTGCGCTGCGCGGTACATGTGCTGTGAG-----CTGGGG 5545
Db |||||
QY 246 GCCGCGCAATGTTCTGTGTCATCACTTGGTTAGCCCTTCGCGTGGTCTGGGTTGT 305
Db |||||
QY 5546 TGTGCGCTGCTCACACGGTGGCGTGGCGTTGCGGCTTCAATTGCTCTTCT 5605
Db |||||
QY 306 CGATATGTTGAGCTCGACAGCGCGTGGAGCGGGAGGCGCACATCCACGAGCCCC 365
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QY 5666 CACAGTGGGCAAGCTCTCTTCGAGGAGATCAGCGGTTGCTGACGCGGTGGAGCGG 5725
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QY 424 GTGTGCCCCGCGGTGCTGAGCGCCAGCATGCGGATCGCGGATCGCGCGATGTTT 483
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QY 5726 CCGGCCACGCTCCGCGCGCACCTCGAGCGCGCGAATCAGCGCGCGGTCTTGATGG 5785
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QY 6266 TACCTGTGTCACGCGCGGTCTCATGTCAGCGCGGTTGTGTGACCAACGATCGACGC 6325
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QY 1021 AGTAGTGTGCGCTCGCAACAGCGACGTACTCGCGCGAGCGCG 1068
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RESULT 13

US-08-713-928B-8/c

; Sequence 8, Application US/08713928B

; Patent No. 5929304

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; GENERAL INFORMATION:
; APPLICANT: RADIN, DAVID N.
; APPLICANT: CRAMER, CAROLE L.
; APPLICANT: OISHI, KAREN K.
; APPLICANT: WEISSENBERN, DEBORAH L.
; TITLE OF INVENTION: PRODUCTION OF LYSOSOMAL ENZYMES IN
; TITLE OF INVENTION: PLANT-BASED EXPRESSION SYSTEMS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/713,928B
; FILING DATE: 13-SEP-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/003,737
; FILING DATE: 14-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7956-0011-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2067 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; US-08-713-928B-8
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Query Match 3.5%; Score 53; DB 2; Length 2067;

Best Local Similarity 48.0%; Pred. No. 0.024;

Matches 182; Conservative 0; Mismatches 195; Indels 2; Gaps 1;

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QY 557 GATGAGCTCTTCGCGCGGGGTCTCCCGGGAACAGGTTCAGCATCGCGTCAAACTGCGC 616
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QY 1260 GACGCCACCGGTGTGTTGCTGTCCAGGACGCTCGCGGCTCGCACACTTCGCGCCAGAG 1201
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QY 617 CGCATGCCCGGACCGCTGCGTCAACAGAACTTTGGCGGCTCCACACTGTTGTGCCA 676
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; Sequence 4, Application US/09191171
; Patent No. 6149909
; Patent No. 6149909 6143294
; GENERAL INFORMATION:
; APPLICANT: SCOTT, Hamish S.
; APPLICANT: ANSON, Donald S.
; APPLICANT: ORSBORN, Annette M.
; APPLICANT: NELSON, Paul V.
; APPLICANT: CLEMENTS, Peter R.
; APPLICANT: MORRIS, Charles P.
; APPLICANT: HOPWOOD, John J.
; TITLE OF INVENTION: SYNTHETIC ALPHA-L-IDURONIDASE AND GENETIC
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY SCOTT MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: USA
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/191,171
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/494,104
; FILING DATE: 23-JUN-1995
; APPLICATION NUMBER: AU PK9490/91
; FILING DATE: 14-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PCT/AU92/00611
; FILING DATE: 12-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/084,254
; FILING DATE: 07-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 8978Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 516-742-4343
; TELEFAX: 516-742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2155 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 89..2047
US-09-191-171-4
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Best Local Similarity 48.0%; Pred. No. 0.025;
Matches 182; Conservative 0; Mismatches 195; Indels 2; Gaps 1;
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677 CATGCTTGGCGTGGCGG 695
1228 CTGCAGTGGCGGGCGG 1210
RESULT 15
US-09-385-707-4/c
; Sequence 4, Application US/09385707
; Patent No. 6238662
; GENERAL INFORMATION:
; APPLICANT: SCOTT, Hamish S.
; APPLICANT: ANSON, Donald S.
; APPLICANT: ORSBORN, Annette M.
; APPLICANT: NELSON, Paul V.
; APPLICANT: CLEMENTS, Peter R.
; APPLICANT: MORRIS, Charles P.
; APPLICANT: HOPWOOD, John J.
; TITLE OF INVENTION: SYNTHETIC ALPHA-L-IDURONIDASE AND GENETIC
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY SCOTT MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: USA
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/385,707
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/494,104
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 8978Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 516-742-4343
; TELEFAX: 516-742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2155 base pairs
; TYPE: nucleic acid
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 89..2047
; US-09-385-707-4

Query Match 3.5%; Score 53; DB 3; Length 2155;
Best Local Similarity 48.0%; Pred.No. 0.025;
Matches 182; Conservative 0; Mismatches 195; Indels 2; Gaps 1;

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Db |||||
QY 1588 CTGCTCTCGCGTGGGAAGACGGCCGGCCAGGCGCCCACTCGCCGTCGGGGCTGCA 1529
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QY 1528 GAGCCCGTTGTCCAGGTAGCGCGTAGACAGGCCCGGGCCGGGGGGCACCCCGCG 1469
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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1119	73.0	1119	7	US-10-388-902-53
5	1119	73.0	1119	7	US-10-647-089-53
6	479.8	31.3	1074	7	US-10-282-122A-28776
7	415.2	27.1	1023	7	US-10-282-122A-25931
8	311	20.3	894	3	US-09-894-844-52
9	311	20.3	894	7	US-10-388-902-52
10	194.4	12.7	366	7	US-10-647-089-52
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12	104.8	6.8	276	7	US-10-282-122A-25902
13	72.8	4.7	951	7	US-10-282-122A-13587
14	65.2	4.3	1395	7	US-10-282-122A-13589
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16	56	3.7	1236	3	US-09-894-844-127
17	56	3.7	1236	7	US-10-388-902-127
18	56	3.7	1236	7	US-10-647-089-127
19	56	3.7	1236	8	US-10-481-265-6
20	55.6	3.6	1544	7	US-10-437-963-7661
21	55.2	3.6	1296	6	US-10-329-027-11
22	54.8	3.6	2196	6	US-10-156-761-5077
23	54.8	3.6	2517	7	US-10-282-122A-25466

ALIGNMENTS

RESULT 1

US-10-259-678-1

; Sequence 1, Application US/10259678

; Publication NO. US20030198974A1

; GENERAL INFORMATION:

; APPLICANT: Cole, Stewart

; APPLICANT: Buchreiser-Brosch, Roland

; APPLICANT: Gordon, Stephen

; APPLICANT: Billault, Alain

; TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM

; TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA

; TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA

; FILE REFERENCE: 3495-0169

; CURRENT APPLICATION NUMBER: US/10/259,678

; CURRENT FILING DATE: 2002-09-30

; PRIOR APPLICATION NUMBER: US/09/060,756

; PRIOR FILING DATE: 1998-04-16

; NUMBER OF SEQ ID NOS: 743

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1

; LENGTH: 12732

; TYPE: DNA

; ORGANISM: Mycobacterium tuberculosis

US-10-259-678-1

Query Match 100.0%; Score 1533; DB 6; Length 12732;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1533; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 11200 ATGTTTCAGCTCGCAACCTCGATCCCGAGGACCTGAAATCCCATCGCGGACCCGACC 11259

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DB 11320 AAGACGGTTTCAGAAATCCCGCGCGCGAGATGAACAGGACGATTCGTCTAACGTGGCG 11379

QY 181 GAGGACTCCGGTATCGTCAAGGTTCCGTCGTGAGGCGAAGCTTGTGGCGGGTGAATTCG 240

DB 11380 GAGGACTCCGGTATCGTCAAGGTTCCGTCGTGAGGCGAAGCTTGTGGCGGGTGAATTCG 11439

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QY 961 TCGTCTTGGGGTGCCGTCGAGGAATGCGACCTGTTGCTTAGCTTCAGCGGATCGATCC 1020
Db 12160 TCGTCTTGGGGTGCCGTCGAGGAATGCGACCTGTTGCTTAGCTTCAGCGGATCGATCC 12219
QY 1021 AGTAGTCTGCTCGCGCTCGCAACACGCGACGTACTCGCCGCGAGCGGCGGACGGGCGCGG 1080
Db 12220 AGTAGTCTGCTCGCGCTCGCAACACGCGACGTACTCGCCGCGAGCGGCGGACGGGCGCGG 12279
QY 1081 TCAGGTTCCATGAGCCGAGGTTTTCGGTCTGAAAGATCGGCGGGAACACGTCGGGGT 1140
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QY 1141 ACCGCTCGCGTACTCACGGATGATCGCGGGGTGCGATCGGTTCGACGCGTCTCGGCGA 1200
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Db 12520 TCACCGTGGGCGCTTTTCTCTGCGCGCGCGAAGGGTATTGGCATGCGCAACGTTGAATCGC 12579
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Db 12580 CTGTGCGCCCGCGCGCGTCTGGCCCTGTGGCTTGGTGGGAGCGTACGGGACACAGCT 12639
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Db 12700 CGCACCGTCTCGAGTCCGCTGGTGGCTCGC 12732

RESULT 2
US-10-282-122A-28775/c
; Sequence 28775, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangshu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28775
; LENGTH: 1122
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-10-282-122A-28775

Query Match 73.2%; Score 1122; DB 7; Length 1122;
Best Local Similarity 100.0%; Pred. No. 1.9e-296;
Matches 1122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 314 TCAGGCTCGACAGCCGCTCGGAGCGGAGGCCACACATCCAGAGCCCTCGGGCT 373
Db 1122 TCAGGCTCGACAGCCGCTCGGAGCGGAGGCCACACATCCAGAGCCCTCGGGCT 1063


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QY 977 GTCGAGGAATCGACCTGTTTCTAGCTTACCGGATCGATCCAGTAGTCTCGCCCTC 1036
DB 459 GTCGAGGAATCGACCTGTTTCTAGCTTACCGGATCGATCCAGTAGTCTCGCCCTC 400
QY 1037 GCACAAACGCGAGTACTCGCCGCGAGCGCGGCACACAGGGCGCGGTCCAGGTTCCTCATTTGAG 1096
DB 399 GCACAAACGCGAGTACTCGCCGCGAGCGCGGCACACAGGGCGCGGTCCAGGTTCCTCATTTGAG 340
QY 1097 GCCGAGGTTTTCGGTCTCGAAGATCGCCGCGGAACACAGTCGCGGTACCCGTCTCGCGGTACTC 1156
DB 339 GCCGAGGTTTTCGGTCTCGAAGATCGCCGCGGAACACAGTCGCGGTACCCGTCTCGCGGTACTC 280
QY 1157 ACGGATGATCGCCGGGTGGCATCGGTGCAACGCTGCTCGGCGACGATGATCTCCACCGG 1216
DB 279 ACGGATGATCGCCGGGTGGCATCGGTGCAACGCTGCTCGGCGACGATGATCTCCACCGG 220
QY 1217 GAAAGTCGGTTTTCTGTCGAGAAAGCTGTCGAAGGCTGACCGGGTACCCCGCTGGTT 1276
DB 219 GAAAGTCGGTTTTCTGTCGAGAAAGCTGTCGAAGGCTGACCGGGTACCCCGCTGGTT 160
QY 1277 GTGAGTGTGCGAGACGATGCTCACCTTGGGGCAAGCTGGGGACTCACCGTCGGCCCTTT 1336
DB 159 GTGAGTGTGCGAGACGATGCTCACCTTGGGGCAAGCTGGGGACTCACCGTCGGCCCTTT 100
QY 1337 TCCTCGCGGCGCGCAAGGTTATTCGATGGCGAAAGCTGTAATCGCTGTCGCCCGCGCGCG 1396
DB 99 TCCTCGCGGCGCGCAAGGTTATTCGATGGCGAAAGCTGTAATCGCTGTCGCCCGCGCGCG 40
QY 1397 TCGGCGCTGTCGGCTTGGTGTGGCGGACGTACGSCAC 1435
DB 39 TCGGCGCTGTCGGCTTGGTGTGGCGGACGTACGSCAC 1
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RESULT 4

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US-10-388-902-53/c
; Sequence 53, Application US/10388902
; Publication No. US20040018574A1
; GENERAL INFORMATION:
; APPLICANT: Behr, Marcel
; APPLICANT: Small, Peter
; APPLICANT: Schoolnik, Gary
; APPLICANT: Wilson, Michael A.
; TITLE OF INVENTION: Molecular Differences Between Species of
; FILE REFERENCE: the M. Tuberculosis Complex
; CURRENT APPLICATION NUMBER: US/10/388,902
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: US/09/894,844
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/318,191
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 60/097,936
; PRIOR FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 1119
; TYPE: DNA
; ORGANISM: Mycobacteria tuberculosis
US-10-388-902-53
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Query Match 73.0%; Score 1119; DB 7; Length 1119;
Best Local Similarity 100.0%; Pred. No. 1.3e-295;
Matches 1119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 317 GCGTCGACAGCGCGTCGAGCGCGGAGCGGCACACATCCAGAGCCCTCGGCTCGG 376
DB 1119 GCGTCGACAGCGCGTCGAGCGCGGAGGGCCACACATCCAGAGCCCTCGGCTCGG 1060
QY 377 CGTCGCGGCGCGAGCTTCGCGCACTGGGTCTTTAGCCCGCGCGGGGTGTCGCCCGCG 436
DB 1059 CGTCGCGGCGCGAGCTTCGCGCACTGGGTCTTTAGCCCGCGCGGGGTGTCGCCCGCG 1000
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RESULT 5

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US-10-647-089-53/c
; Sequence 53, Application US/10647089
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QY 437 GTGCTGACAGCGCAGATGGCGATCGGGGATGGCGCGCGATGGTTTCTCTGAGCCCGCG 496
DB 999 GTGCTGACAGCGCAGATGGCGATCGGGGATGGCGCGCGATGGTTTCTCTGAGCCCGCG 940
QY 497 GGGCCCTTCCGGGCTTGGAAAGCTTGGCGATCTGGCGGAAGGATCCAGTGGCGCATGACGC 556
DB 939 GGGCCCTTCCGGGCTTGGAAAGCTTGGCGATCTGGCGGAAGGATCCAGTGGCGCATGACGC 880
QY 557 GATGAGTCTCTCGCGCGCGGGGTCTCCCGGGGAACAGGTGAGCATCGCGTCAAAACGTGCG 616
DB 879 GATGAGTCTCTCGCGCGCGGGGTCTCTCCCGGGGAACAGGTGAGCATCGCGTCAAAACGTGCG 820
QY 617 CGCATGCCCGCGACCTTGGCTCAACAGAACTTTTGGCGGGTCCACCACTGGTTGTGCCA 676
DB 819 CGCATGCCCGCGACCTTGGCTCAACAGAACTTTTGGCGGGTCCACCACTGGTTGTGCCA 760
QY 677 CATGCTTTGGGCGTGGCGCGATACACGCCATGGTGTGGGCAACATGGCGATGTGCGC 736
DB 759 CATGCTTTGGGCGTGGCGCGATACACGCCATGGTGTGGGCAACATGGCGATGTGCGC 700
QY 737 ATGCAACCGCGTCCCGGACGTGCGATACCAAGTCCAGGGGCGATGAGTCCGCGAGGAATGTC 796
DB 699 ATGCAACCGCGTCCCGGACGTGCGATACCAAGTCCAGGGGCGATGAGTCCGCGAGGAATGTC 640
QY 797 GTGCTAGGCTCGAGCGCGACGTGACCGCGAGTTGGTCTCGATGAAGTTCATCAAGAT 856
DB 639 GTGCTAGGCTCGAGCGCGACGTGACCGCGAGTTGGTCTCGATGAAGTTCATCAAGAT 580
QY 857 CAACGCATCCAGGCTCAAGTTGCCCGCACCCGAAACCGGGGGAACTTCGAGTCTTGGC 916
DB 579 CAACGCATCCAGGCTCAAGTTGCCCGCACCCGAAACCGGGGGAACTTCGAGTCTTGGC 520
QY 917 ATGGCGCTCTCCCATATCATCTCGACGGGATGGAAGCACACCGTCTTGGGGTGGCG 976
DB 519 ATGGCGCTCTCCCATATCATCTCGACGGGATGGAAGCACACCGTCTTGGGGTGGCG 460
QY 977 GTGAGGAATGCGACTGTTTGTAGTTTACGCGGATCGATCCAGTAGTCTCGCCCTC 1036
DB 459 GTGAGGAATGCGACTGTTTGTAGTTTACGCGGATCGATCCAGTAGTCTCGCCCTC 400
QY 1037 GCACAAACGCGAGTACTCGCGCGAGCGCGCACAGGGCGCGGTCCAGGTTCCTCATTTGAG 1096
DB 399 GCACAAACGCGAGTACTCGCCGCGAGCGCGCACAGGGCGCGGTCCAGGTTCCTCATTTGAG 340
QY 1097 GCCGAGGTTTTCGGTCTCGAAGATCGCCGCGGAACACAGTCGCGGTACCCGTCTCGCGTACTC 1156
DB 339 GCCGAGGTTTTCGGTCTCGAAGATCGCCGCGGAACACAGTCGCGGTACCCGTCTCGCGTACTC 280
QY 1157 ACGGATGATCGCCGGGTGGCATCGGTGCAACGCTGCTCGGCGACGATGATCTCCACCGG 1216
DB 279 ACGGATGATCGCCGGGTGGCATCGGTGCAACGCTGCTCGGCGACGATGATCTCCACCGG 220
QY 1217 GAAAGTCGGTTTTCTGTCGAGAAAGCTGTCGAAGGCTGACCGGGGTAGCCCGCTGGTT 1276
DB 219 GAAAGTCGGTTTTCTGTCGAGAAAGCTGTCGAAGGCTGACCGGGGTAGCCCGCTGGTT 160
QY 1277 GTGAGTGTGCGAGACGATGCTCACCTTGGGGCAAGCTGGGGACTCACCGTCGGCCCTTT 1336
DB 159 GTGAGTGTGCGAGACGATGCTCACCTTGGGGCAAGCTGGGGACTCACCGTCGGCCCTTT 100
QY 1337 TCCTCGCGGCGCGCAAGGTTATTCGATGGCGAAAGCTGTAATCGCTGTCGCCCGCGCGCG 1396
DB 99 TCCTCGCGGCGCGCAAGGTTATTCGATGGCGAAAGCTGTAATCGCTGTCGCCCGCGCGCG 40
QY 1397 TCGGCGCTGTCGGCTTGGTGTGGCGGACGTACGSCAC 1435
DB 39 TCGGCGCTGTCGGCTTGGTGTGGCGGACGTACGSCAC 1
```


Db 719 CCGGACCCCTGCATCCGACAGAGGTGGCCGGATCGGTGATCGACTTGTACCATGCGCG 660
Qy 684 TGGCGGTGGCGGATACAGCGGCATGGTTCGGGACACATGCGGATGCGCATGACC 743
Db 659 CGCGGGTGGCGGATAGACCGGCATCGTCTCCGGCAGCATGCGGATGGCGCTTCGGCG 600
Qy 744 GCGTGGCGGACGTGCAGATACACAGTCCAGGGGATGACGTCCGCGAGAAATGTCGTGTAG 803
Db 599 GCATGCGGACGTGCAGGTACAGTCCAGGGGATGACATCGCGCGGATGTCGTGTAG 540
Qy 804 CGCTCAGGCGACGCGTACAGCGCGGATGGTCTGGATGAAGTTCATCAAGATCAACGCA 863
Db 539 CGCGGAGGCGCGGTACATACCGAGTTGGTCTGGATGAAGTTGCGGAGATCAGCGTC 480
Qy 864 TCAGGCTCAAGTTGGTCCCGCACCCGACCGGGGGGAACTTTGGCGAGGAATCTCTTCG 420
Db 479 TCGAAGCTGAGGTTCACCCGCGCGGAGGCGCGGAACTTTGGCGAGGAATCTCTTCG 420
Qy 903 TCGAGTCCCTTGGCATGGCGGCTCTCCCATATC 935
Db 419 AACTTCGGATACAGGTGTGGACGAGTTCTCTCTCCGCGACATCTGTGGGTCCAGACC 360
Qy 936 ACTCGACCGGATGGAAGCACACCGTGTCTGGGGTGGCGGTTCGAGGAATGCGACCTGT 995
Db 359 ACCTGCACCGGTGGAACACACCGTGTGTGGGATCTTCGTCCAGCAAGCCACTTGT 300
Qy 996 TTGCTTAGCTTACGCGGATCGATCCAGTAGTCTCGCGCTCGCACAAAGGAGTACTCG 1055
Db 299 TTGGTCAGTTTCAACGGGTGCAGCAGTAGTCTCGCGCTCGCACAGCGGATGTACTCG 240
Qy 1056 CCGCGAGCGCGCACAGGGCGCGGTTCAGTTCCCATGAGGCGGAGTTTTCGGTCCGTG 1115
Db 239 CCACGCGCGCGACAGGGCACCGGTGAGGTGGCGGTGAGGCGGACGTTTTCGACCGC 180
Qy 1116 AAGATCGCGCGAACAGTGCAGGTACCGTTCGGCGTACTTCAGGATGATCGCGGGGTG 1175
Db 179 AGGATCGCGCGAAGAGTTTCGATGCGCGTGGCGGTAGTCTCGGATGATTCGGGGTGTG 120
Qy 1176 GCATCGGTGACCGCTGTCGGCGGACGATGATCTCACCGGGAAGTCGGTTGCTGCTGTCG 1235
Db 119 GCATCGGTGAGGCATCGTGGCGACGATGACCTCCATCGGAAAGTCGACCCGCTGGGG 60
Qy 1236 AGAAGCTGTGGAAGCCTGACGGGCGTAGCCGCTGTTGAGTGTGAGTGTGAGACGA 1293
Db 59 AGAAGCGGTCCAACGTTCGCGGACATAGGCGTCTGTTGTTGGGTGTGACACCA 2

RESULT 8
US-09-894-844-52/c
; Sequence 52, Application US/09894844
; Patent No. US20020176873A1
; GENERAL INFORMATION:
; APPLICANT: Behr, Marcel
; APPLICANT: Small, Peter
; APPLICANT: Schoolnik, Gary
; APPLICANT: Wilson, Michael A.
; TITLE OF INVENTION: Molecular Differences Between Species of
; FILE REFERENCE: STAN102CON
; CURRENT APPLICATION NUMBER: US/09/894,844
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/318,191
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 60/097,936
; PRIOR FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 894
; TYPE: DNA
; ORGANISM: Mycobacteria tuberculosis
US-09-894-844-52

Query Match 20.3%; Score 311; DB 3; Length 894;
Best Local Similarity 100.0%; Pred. No. 8e-75; 0; Indels 0; Gaps 0;
Matches 311; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGTTTCAGCTCGCGAACCTTCGATCCCGAGGACCTGAAATCCCATGCGCGGAAACCGGACC 60
Db 311 ATGTTTCAGCTCGCGAACCTTCGATCCCGAGGACCTGAAATCCCATGCGCGGAAACCGGACC 252
Qy 61 GCGTACCCGCCCTTCGAGCAGCGGACATCGGCGAGCGGTAGTGGCTCTTGTCCCGGGA 120
Db 251 GCGTACCCGCCCTTCGAGCAGCGGACATCGGCGAGCGGTAGTGGCTCTTGTCCCGGGA 192
Qy 121 AAGACGGTTTCCAGAAATCCCGCGCGGAGATGAACAGGACGATTCGTCTAACGTGCGC 180
Db 191 AAGACGGTTTCCAGAAATCCCGCGCGGAGATGAACAGGACGATTCGTCTAACGTGCGC 132
Qy 181 GAGGACTCCGGTATCGTCAAGGTTCCGTCGTGAGGCGGAAACGTTGTGGCGGTGAATTGT 240
Db 131 GAGGACTCCGGTATCGTCAAGGTTCCGTCGTGAGGCGGAAACGTTGTGGCGGTGAATTGT 72
Qy 241 ACGCGCGCGCGGATGTTCTGTGCGCATCACTTGTGAGCCCTTCGGCTGCTCTGGG 300
Db 71 ACGCGCGCGCGGATGTTCTGTGCGCATCACTTGTGAGCCCTTCGGCTGCTCTGGG 12
Qy 301 TTTGTCGACAT 311
Db 11 TTTGTCGACAT 1
RESULT 9
US-10-388-902-52/c
; Sequence 52, Application US/10388902
; Publication No. US20040018574A1
; GENERAL INFORMATION:
; APPLICANT: Behr, Marcel
; APPLICANT: Small, Peter
; APPLICANT: Schoolnik, Gary
; APPLICANT: Wilson, Michael A.
; TITLE OF INVENTION: Molecular Differences Between Species of
; FILE REFERENCE: STAN102CON
; CURRENT APPLICATION NUMBER: US/10/388,902
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: US/09/894,844
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/318,191
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 60/097,936
; PRIOR FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 894
; TYPE: DNA
; ORGANISM: Mycobacteria tuberculosis
US-10-388-902-52
Query Match 20.3%; Score 311; DB 7; Length 894;
Best Local Similarity 100.0%; Pred. No. 8e-75;
Matches 311; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGTTTCAGCTCGCGAACCTTCGATCCCGAGGACCTGAAATCCCATGCGCGGAAACCGGACC 60
Db 311 ATGTTTCAGCTCGCGAACCTTCGATCCCGAGGACCTGAAATCCCATGCGCGGAAACCGGACC 252
Qy 61 GCGTACCCGCCCTTCGAGCAGCGGACATCGGCGAGCGGTAGTGGCTCTTGTCCCGGGA 120
Db 251 GCGTACCCGCCCTTCGAGCAGCGGACATCGGCGAGCGGTAGTGGCTCTTGTCCCGGGA 192
Qy 121 AAGACGGTTTCCAGAAATCCCGCGCGGAGATGAACAGGACGATTCGTCTAACGTGCGC 180
Db 191 AAGACGGTTTCCAGAAATCCCGCGCGGAGATGAACAGGACGATTCGTCTAACGTGCGC 132

QY 181 GAGGACTCGGTATCGTCAAGGTTCCGTGCTGAGCGGAACCTTGTGGCGGTGAATTGT 240
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
131 GAGGACTCGGTATCGTCAAGGTTCCGTGCTGAGCGGAACCTTGTGGCGGTGAATTGT 72
QY 241 ACCGGCCCGCGGAATGTTCTGTGTGCATCACTTGGTTAGCCCTTCGGCTGCTCTGGG 300
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
71 ACCGGCCCGCGGAATGTTCTGTGTGCATCACTTGGTTAGCCCTTCGGCTGCTCTGGG 12
QY 301 TTTGTGACAT 311
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
11 TTTGTGACAT 1

RESULT 10

US-10-647-089-52/c

; Sequence 52, Application US/10647089

; Publication No. US20040063923A1

; GENERAL INFORMATION:

; APPLICANT: Behr, Marcel

; APPLICANT: Small, Peter

; APPLICANT: Schoolnik, Gary

; APPLICANT: Wilson, Michael A.

; TITLE OF INVENTION: Molecular Differences Between Species of

; FILE REFERENCE: STAN102CON

; CURRENT APPLICATION NUMBER: US/10/647,089

; PRIOR FILING DATE: 2003-08-21

; PRIOR APPLICATION NUMBER: US/09/894,844

; PRIOR FILING DATE: 2001-06-27

; PRIOR APPLICATION NUMBER: 09/318,191

; PRIOR FILING DATE: 1999-05-25

; PRIOR APPLICATION NUMBER: 60/097,936

; PRIOR FILING DATE: 1998-08-25

; NUMBER OF SEQ ID NOS: 137

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 52

; LENGTH: 894

; TYPE: DNA

; ORGANISM: Mycobacteria tuberculosis

US-10-647-089-52

Query Match 20.3%; Score 311; DB 7; Length 894;
Best Local Similarity 100.0%; Pred. No. 8e-75; Indels 0; Gaps 0;
Matches 311; Conservative 0; Mismatches 0;

QY 1 ATGTTTCAGCTCGGAACCTCGATCCGAGGACCTGAAATCCCATGCGCGGAACCGACC 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
311 ATGTTTCAGCTCGGAACCTCGATCCGAGGACCTGAAATCCCATGCGCGGAACCGACC 252
QY 61 GGTATCCCGCTTCCAGCAGCGGACATCGGCGAGCGTAGTGCTTTGTCCCGGGA 120
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
251 GGTATCCCGCTTCCAGCAGCGGACATCGGCGAGCGTAGTGCTTTGTCCCGGGA 192
QY 121 AAGAGGTTTCCAGAAATCCCGCGCGGAGATGAACAGGACGATTTCGCTAACGTCGCG 180
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
191 AAGAGGTTTCCAGAAATCCCGCGCGGAGATGAACAGGACGATTTCGCTAACGTCGCG 132
QY 181 GAGGACTCCGGTATCGTCAAGGTTCCGTGCTCGAGCGGAACGTTGTGGCGGTGAATTGT 240
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
131 GAGGACTCCGGTATCGTCAAGGTTCCGTGCTCGAGCGGAACGTTGTGGCGGTGAATTGT 72
QY 241 ACCGGCCCGCGGAATGTTCTGTGTGCATCACTTGGTTAGCCCTTCGGCTGCTCTGGG 300
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
71 ACCGGCCCGCGGAATGTTCTGTGTGCATCACTTGGTTAGCCCTTCGGCTGCTCTGGG 12
QY 301 TTTGTGACAT 311
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
11 TTTGTGACAT 1

RESULT 11

US-10-282-122A-26084/c

; Sequence 26084, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Hasselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26084
; LENGTH: 366
; TYPE: DNA
; ORGANISM: Mycobacterium avium
US-10-282-122A-26084

Query Match 12.7%; Score 194.4; DB 7; Length 366;
Best Local Similarity 73.7%; Pred. No. 5.6e-43;
Matches 261; Conservative 0; Mismatches 91; Indels 2; Gaps 1;
QY 943 CGGGATGGAAGCACACCGTCGTCTT--GGGGTGCCTGCGAGGAATGCGACCTGTTTGT 1000
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
354 CGGGGTGGAACACACACCGTGTGTGTCGGGATCTCTCGAGCCCGCCACTGTTTGT 295
QY 1001 TAGCTTACAGCGATCGATCCAGTAGTCTGCCCTCGACAACGCGACGTACTCGCCGG 1060
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
294 CAATTTCAACGGGTGACCCAGTAGTCTGCGCCCTCGCACAGCGGATGACTCGCCACG 235
QY 1061 AGCGGCCGACAGGGCGCGGTTCAGGTTCCTATTGAGGCCGAGGTTTTCGGTCTCGAAGAT 1120
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
234 CGCGCGGACAGGGCACCGGTGAGGTGGCGTTGAGGCCGAGCTTCTCGACCGCAGGAT 175
QY 1121 CGCGCGGAACACGTGCGGGTACCGCTCGGCGGTACTCACGGATGATCGCGGGTGGCATC 1180
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
174 GGGCCGGAAGAGTTTCGGATGCGGTGCGCGGTATCTCTGATGATTTCGGGGTGGCATC 115
QY 1181 GGTTCAGCGGTCTGTCGGCGACGATGATCTCCACCGGGAAGTCGGTTTGTGTCGAGAA 1240
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
114 GGTTCAGGCGATCTGTCGGGACTATTACCTCCATCGAAAAGTCTACCCGCTGGCGAGAA 55
QY 1241 GCTGTGGAAGGCTTCAGCGGCGTAGCCCGCTGGTGTGTGAGTGGTTCGAGACGAT 1294

RESULT 14

US-10-282-122A-35893/c
; Sequence 35893, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangou
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35893
; LENGTH: 1395
; TYPE: DNA
; ORGANISM: Streptococcus mutans
US-10-282-122A-35893

Query Match 4.3%; Score 65.2; DB 7; Length 1395;
Best Local Similarity 50.0%; Pred. No. 1.2e-07;
Matches 163; Conservative 0; Mismatches 163; Indels 0; Gaps 0;
QY 978 TCAGGAATGCACCTGTTTGGCTTAGCTTCAGCGGATCGATCGAGTAGTCGTCGCGCTG 1037
DB 332 TCTAAAGATCAATTTGTTTGAAGCTTAAAGGCTCTCAATAATCATCACCATCA 273
QY 1038 CACAACGCGACCTACTCGCGCGAGCGCGGCGGCTCAGGTTCCCATTTGAGG 1097
DB 272 CATCTGGCAATGACTGTCTCTAGCTTTCTACAAATATCGACCAAGTTTGTGTAAT 213
QY 1098 CCGAGGTTTTCGGTCTGGAAGATCGCGCGGAACAGCTGCGGGTACCGCTCGCGGTACTCA 1157
DB 212 CCTTGATTCTTGTGTTAAAGAAAGCCGCAATTAATCTGGATCTGTTTTGTATAGGTT 153
QY 1158 CGGATGATCGCGGGTGCATCGGTTCGACGCTGTCGGCGACGATGATCTCCACCGG 1217
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QY 1218 AAGTCGGTTTGTGTCGAGAAAGCTGTCGAAGGCTGACGGGCGGTAGCCGCTGGTTG 1277
DB 92 AATGATGTTTCTGTTTTCAGGAACCTATCAATAGCTTCCCAATCCAGTTCCTTTATTA 33

QY 1278 TCAGTGGTCGACGACGATGCTACCTT 1303
DB 32 TAAATGGTCGCAAAATAATGATACTTT 7

RESULT 15

US-09-976-059-1/c
; Sequence 1, Application US/09976059
; Patent No. US2002016474A1
; GENERAL INFORMATION:
; APPLICANT: Farnet, Chris
; APPLICANT: Zazopoulos, Emmanuel
; APPLICANT: Staffa, Alfredo
; TITLE OF INVENTION: Genes and Proteins for Biosynthesis of Ramoplanin
; FILE REFERENCE: 3019-PCT
; CURRENT APPLICATION NUMBER: US/09/976,059
; CURRENT FILING DATE: 2001-10-15
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 88421
; TYPE: DNA
; ORGANISM: Actinoplanes sp.
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; LOCATION: (2077)..(3078)
; OTHER INFORMATION: ORF 1; positive strandedness
; NAME/KEY: misc.feature
; LOCATION: (3118)..(4032)
; OTHER INFORMATION: ORF 2; positive strandedness
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; NAME/KEY: misc.feature
; LOCATION: (4038)..(5048)
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; LOCATION: (65826)..(66530)
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; OTHER INFORMATION: ORF 25; negative strandedness
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; LOCATION: (81624)..(79861)
; OTHER INFORMATION: ORF 26; negative strandedness
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; LOCATION: (84481)..(85548)
; OTHER INFORMATION: ORF 30; positive strandedness
; NAME/KEY: misc_feature
; LOCATION: (85556)..(86845)
; OTHER INFORMATION: ORF 31; positive strandedness
; NAME/KEY: misc_feature
; LOCATION: (87372)..(86803)
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; OTHER INFORMATION: ORF 33; positive strandedness; N-terminus only
US-09-976-059-1

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Matches 262; Conservative 0; Mismatches 341; Indels 0; Gaps 0;

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QY      733  CGCCATGCAACCGCGTCCGCGACGTGCAGATACAGTCCAGGGGCATGACGTCCGCGAGGAA 792
DB      40760  CCACCTGGAAACAGCGGTGGCGCTCAGCGACCGCGACGCGCGAGCTCTCTGACGAGCT 40701

QY      793  TGTCTGCTAGCGCTCAGGCGGACGCTACACGCCCGAGTGTGCTCGATGAGTTTCATCA 852
DB      40700  TCTCGAACCGGACGCTCTGTGGCCGCTACGCGTTCGAGGGGCCGCTCGCGGACCTGCGCGCA 40641

QY      853  AGATCAACGATCCAGGCTCAAGTTGCCCGCGCACCCGAAACCGGGGGGAACTTCGAGTCTCT 912
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DB      40580  AGCAGCCGACGAGGTCTGTCAGGCCCGGCTCGGTGCGCGCGGCCACACCGTCCCGATCG 40521
QY      973  GCGGTTCGAGGAATGCGACTGTTTCTTAGCTTCAGCGGATCGATCCAGTACGTCTGTCGG 1032
DB      40520  GCAGGTCTGTCGCGCGCGCCAGCGCGGAAGACACATGGGGTTCGCGCGGTGCACGGCCA 40461
QY      1033  CCTCGCACAAACGCGACGTACTCGCCCGGACGCGCGCGGCGCGCGGTTCAGGTTCCTCAT 1092
DB      40460  TGAAGAGCGTGGCGCGAGCTCGCGGTGAGGGCGGTTCAGGTTCGCGGTGGCGCGCGCG 40401
QY      1093  TGAGCGCGAGGTTTTCGGTCTCTGAAGATCGGCGCGGAACAGTTCGGGTACCGTTCGGCGT 1152
DB      40400  GCACGCGCAACTCGGCGCATGTGCGCGCGGACGACGACGCGGCGCGCGCGTGTGTCGG 40341
QY      1153  ACTCACGGATGATCGCGGGGTGGCATCGGTTCGACGCGTCTCGGCGACGATGATCTCCA 1212
DB      40340  CCGGCGGCGCGAGCTCTCGGGGCTTCGCGGAGCGCGCGCAATAGCCGACCTGCT 40281
QY      1213  CCGGGAAGTTCGGTTCGTTCGAGAAAGCTGTTCGAAAGCCTTCGACGGGCGTACGCCGCT 1272
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QY      1273  GGT 1275
DB      40220  AGT 40218
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Job time : 1324.13 secs

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GenCore version 5.1.7
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Run on: February 20, 2006, 01:43:06 ; Search time 500.571 Seconds
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6500.886 Million cell updates/sec

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Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 7204252 seqs, 1061369211 residues

Total number of hits satisfying chosen parameters: 14408504

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications NA New:*

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- 2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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- 11: /cgn2_6/ptodata/1/pubpna/US16_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US17_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US18_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1533	100.0	12732	8	US-10-802-796-1
2	1119	73.0	1119	12	US-11-143-401-53
3	311	20.3	894	12	US-11-143-401-52
4	57.4	3.7	88421	12	US-11-205-109-1
5	56	3.7	1236	12	US-11-143-401-127
6	53	3.5	2155	12	US-11-122-329-122
7	53	3.5	2937	9	US-11-202-566-8
8	53	3.5	6200	8	US-10-895-011-1
9	53	3.5	6200	12	US-11-038-372-1
10	53	3.5	37500	8	US-10-522-037-1
11	49.6	3.2	1386	8	US-10-858-730-133
12	47.2	3.1	10968	12	US-11-075-185-35
13	47.2	3.1	78869	12	US-11-075-185-1
14	45.4	3.0	1356	12	US-11-024-959-78
15	45	2.9	5679	12	US-11-075-185-36
16	44.8	2.9	897	8	US-10-432-483-3
17	44.8	2.9	3624	7	US-10-755-092-6
18	44.8	2.9	8651	8	US-10-432-483-48
19	44.6	2.9	5301	12	US-11-075-185-40
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c 21	43.8	2.9	607	6	US-09-925-065A-830710	Sequence 830710,
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c 24	43.4	2.8	607	6	US-09-925-065A-762705	Sequence 762705,
c 25	43.4	2.8	614	6	US-09-925-065A-770570	Sequence 770570,
c 26	42.8	2.8	4509	12	US-11-087-100-5	Sequence 5, Appli
c 27	42.8	2.8	4509	12	US-11-087-084-5	Sequence 5, Appli
c 28	42.8	2.8	4509	12	US-11-087-085-5	Sequence 5, Appli
c 29	42.6	2.8	37507	8	US-10-522-037-2	Sequence 2, Appli
c 30	42.2	2.8	5121	8	US-10-775-169-319	Sequence 319, App
c 31	42	2.7	1119	8	US-10-858-730-48	Sequence 48, Appl
c 32	41.6	2.7	912	8	US-10-432-483-15	Sequence 15, Appl
c 33	41.6	2.7	8651	8	US-10-432-483-48	Sequence 48, Appl
c 34	41.2	2.7	14172	12	US-11-075-185-2	Sequence 2, Appli
c 35	41	2.7	1629	8	US-10-858-730-177	Sequence 177, App
c 36	40.8	2.7	990	7	US-10-714-887-115	Sequence 115, App
c 37	40.8	2.7	2302	12	US-11-110-082-20	Sequence 20, Appl
c 38	40.6	2.6	546	12	US-11-089-945-4	Sequence 4, Appli
c 39	40.6	2.6	4551	8	US-10-220-824-7	Sequence 7, Appli
c 40	40.6	2.6	88421	12	US-11-205-109-1	Sequence 1, Appli
c 41	40.4	2.6	1400	12	US-11-136-527-7054	Sequence 7054, Ap
c 42	40.4	2.6	2186	12	US-11-136-527-2958	Sequence 2958, Ap
c 43	40.4	2.6	3513	8	US-10-858-730-142	Sequence 142, App
c 44	40.2	2.6	978	12	US-11-143-980-18	Sequence 18, Appl
c 45	40.2	2.6	11070	12	US-11-075-185-34	Sequence 34, Appl

ALIGNMENTS

RESULT 1

US-10-802-796-1
; Sequence 1, Application US/10802796
; Publication No. US20050250104A1
; GENERAL INFORMATION:
; APPLICANT: COLE, STEWART
; APPLICANT: BUCHRIER-BROSCH, ROLAND
; APPLICANT: GORDON, STEPHEN
; APPLICANT: BILLAULT, ALAIN
; TITLE OF INVENTION: A METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST
; TITLE OF INVENTION: FROM THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED
; TITLE OF INVENTION: DNA LIBRARY. APPLICATION TO THE DETECTION OF
; TITLE OF INVENTION: MYCOBACTERIA.
; FILE REFERENCE: 05394.0011-00000
; CURRENT APPLICATION NUMBER: US/10/802,796
; PRIOR FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: US/09/673,476
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: PCT/IB99/00740
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 09/060,756
; PRIOR FILING DATE: 1998-04-16
; NUMBER OF SEQ ID NOS: 743
; SOFTWARE: PatentIn Ver. 2.2
; SEQ ID NO 1
; LENGTH: 12732
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-10-802-796-1

Query Match	100.0%;	Score 1533;	DB 8;	Length 12732;
Best Local Similarity	100.0%;	Pred. No. 0;		
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Qy	1	ATGTTTCAGCTCGGAACCTCGATCCCGAGGACCTGAAATCCCATGCGCGGAACCCGACC	60	
Db	11200	ATGTTTCAGCTCGGAACCTCGATCCCGAGGACCTGAAATCCCATGCGCGGAACCCGACC	11259	
Qy	61	GGTACCCGCTTCCAGCAGCGGATCGGCGGAGCTAGTGGCTCTTGTCCCGGGA	120	
Db	11260	GGTACCCGCTTCCAGCAGCGGATCGGCGGAGCTAGTGGCTCTTGTCCCGGGA	11319	
Qy	121	AAGACGGTTTCCAGAAATCCCGCGCGGAGATGAACAGGACGATTCTGCTTAACGTGCGC	180	

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Db 11440 ACCGCGCGCGCGAATGTTCTGTGCGCATCACTTGTGTAAGCCCTTCGGGCTGCTCGGG 11499
QY 301 TTTGTGCAATGTCAGGTCGACAGCCGCTCGAGCGCGGAGGSCACACATCCACGA 360
Db 11500 TTTGTGCAATGTCAGGTCGACAGCCGCTCGAGCGCGGAGGSCACACATCCACGA 11559
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Db 11560 GCGCCCTCGGGTTCGGCGTCGCGCGCGGAGCTTCGCCCACTGGGTCCTTTGAGCGCGCGG 11619
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Db 11680 TTTCTGTGAGCGCGCGCGCCCTTCGCGGCTTGGAAACGTTGGCGATCTGCGCAAGGATCC 11739
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Db 11980 CGTCGCGAGAAATGTCGTGAGCGTCCAGCGGACGGTACACGGCCGAGTTGGTCTGGA 12039
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QY 1381 CTGTGCGCCCGCGCGCTCGCGCGCTGTGCGCTGGTGGCGGACGTAACGACACGCT 1440
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QY 1441 GCGGAAGTATACGAGGGTGCATGACGTTGGGCTCGAAACCGGTCGCGCGGTTGGG 1500
Db 12640 GCGGAAGTATACGAGGGTGCATGACGTTGGGCTCGAAACCGGTCGCGCGGTTGGG 12699
QY 1501 GCGACGCTCTCAGGTCGGTCTGCTGGTGGCTCGC 1533
Db 12700 GCGACGCTCTCAGGTCGGTCTGCTGGTGGCTCGC 12732

RESULT 2

US-11-143-401-53/C
; Sequence 53, Application US/11143401
; Publication NO. US20060002953A1
; GENERAL INFORMATION:
; APPLICANT: Behr, Marcel
; APPLICANT: Small, Peter
; APPLICANT: Schoolnik, Gary
; APPLICANT: Wilson, Michael A.
; TITLE OF INVENTION: Molecular Differences Between Species of
; TITLE OF INVENTION: the M. Tuberculosis Complex
; FILE REFERENCE: STAN102CON
; CURRENT APPLICATION NUMBER: US/11/143,401
; CURRENT FILING DATE: 2005-06-01
; PRIOR APPLICATION NUMBER: US/10/647,089
; PRIOR FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: US/09/894,844
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/318,191
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 60/097,936
; PRIOR FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 1119
; TYPE: DNA
; ORGANISM: Mycobacteria tuberculosis
US-11-143-401-53

Query Match 73.0%; Score 1119; DB 12; Length 1119;
Best Local Similarity 100.0%; Pred. No. 3.7e-278; Mismatches 0; Indels 0; Gaps 0;
Matches 1119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 377 CGTCGCGCGCGGAGCTTCGCGCACTGGGTCTTTAGCGCGCGCGGGGTGTGCCCCCGCG 436
Db 1059 CGTCGCGCGCGGAGCTTCGCGCACTGGGTCTTTAGCGCGCGCGGGGTGTGCCCCCGCG 1000
QY 437 GTGCTGCAAGCGCCAGCATGGCGATCCGGGATGGCGCGATGTTCTTCGAGCGCGCG 496
Db 999 GTGCTGCAAGCGCCAGCATGGCGATCCGGGATGGCGCGATGTTCTTCGAGCGCGCG 940
QY 497 GCGCCCTCTCGGGCCTTGGAAACGTTGGCGATCTGGGCGAAGGATCCAGTCCGGCCATGACGCG 556
Db 939 GCGCCCTCTCGGGCCTTGGAAACGTTGGCGATCTGGGCGAAGGATCCAGTCCGGCCATGACGCG 880

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QY 617 CGCATGCCCGGACCCCTGCGTCAACAGAACTTTGGCGGGTCCACACCTGGTGTGGCCA 676
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QY 737 ATGCACCGCTGCGGACGTGACAGATACAGTCCAGGGGATGACGTGCGCAGGAATGTC 796
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QY 917 ATGGCGCTCTCCCATATCACTCGGACGGGATGGAAGCACACCGTCTGTGGGGTGCCG 976
Db 519 ATGGCGCTCTCCCATATCACTCGGACGGGATGGAAGCACACCGTCTGTGGGGTGCCG 460
QY 977 GTCGAGGAATGCACTGTTGCTTAGCTTACGGGATCGATCCAGTAGTCTGTCGCGCTC 1036
Db 459 GTCGAGGAATGCACTGTTGCTTAGCTTACGGGATCGATCCAGTAGTCTGTCGCGCTC 400
QY 1037 GCACAAACGCGACGTACTCGCGCGAGCGCGCGACAGGGCGCTCAGGTTCCCATTTAG 1096
Db 399 GCACAAACGCGACGTACTCGCGCGAGCGCGCGACAGGGCGCTCAGGTTCCCATTTAG 340
QY 1097 GCCGAGTTTTTGGTCTCTGAAGATCGGCGGAAACACGTGCGGGTACCGTCTCGCGTACTC 1156
Db 339 GCCGAGTTTTTGGTCTCTGAAGATCGGCGGAAACACGTGCGGGTACCGTCTCGCGTACTC 280
QY 1157 ACGGATGATCGCGGGGTGCGATCGGTGACGCGGTGTGCGGACAGATGATCTCCACGG 1216
Db 279 ACGGATGATCGCGGGGTGCGATCGGTGACGCGGTGTGCGGACAGATGATCTCCACGG 220
QY 1217 GAAGTCGTTTTGCTGTCGAGAAAGCTGTGCGAGGCTGACGGGCTGAGCGCGCTGGTT 1276
Db 219 GAAGTCGTTTTGCTGTCGAGAAAGCTGTGCGAGGCTGACGGGCTGAGCGCGCTGGTT 160
QY 1277 GTGAGTGTGTCGACAGATGCTACCTTTGGGGCAAGCTGGGGACTCACCGTTCGGCCCTTT 1336
Db 159 GTGAGTGTGTCGACAGATGCTACCTTTGGGGCAAGCTGGGGACTCACCGTTCGGCCCTTT 100
QY 1337 TCGTGGCGGCGCGAAGGTTATTCGATGCGGAACTGTAATGCCCTGTGCGCGCGCGCG 1396
Db 99 TCGTGGCGGCGCGAAGGTTATTCGATGCGGAACTGTAATGCCCTGTGCGCGCGCGCG 40
QY 1397 TCGGCGCTGTGCGCTGTTGTCGCGGAGCTAGCGAC 1435
Db 39 TCGGCGCTGTGCGCTGTTGTCGCGGAGCTAGCGAC 1
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RESULT 3

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US-11-143-401-52/c
; Sequence 52, Application US/11143401
; Publication No. US2006002953A1
; GENERAL INFORMATION:
; APPLICANT: Behr, Marcel
; APPLICANT: Small, Peter
; APPLICANT: Schoolnik, Gary
; APPLICANT: Wilson, Michael A.
; TITLE OF INVENTION: Molecular Differences Between Species of
; TITLE OF INVENTION: the M. Tuberculosis Complex
; FILE REFERENCE: STAN102CON
```

```
; CURRENT APPLICATION NUMBER: US/11/143,401
; CURRENT FILING DATE: 2005-06-01
; PRIOR APPLICATION NUMBER: US/10/647,089
; PRIOR FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: US/09/894,844
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/318,191
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 60/097,936
; PRIOR FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 894
; TYPE: DNA
; ORGANISM: Mycobacteria tuberculosis
; US-11-143-401-52
```

```
Query Match 20.3%; Score 311; DB 12; Length 894;
Best Local Similarity 100.0%; Pred. No. 1.5e-70;
Matches 311; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTTTCAGCTCGGAACTTCGATCCCGAGGACCTGAAATCCCATGCGCGCAACCCGACC 60
Db 311 ATGTTTCAGCTCGGAACTTCGATCCCGAGGACCTGAAATCCCATGCGCGCAACCCGACC 252
QY 61 GCGTACCCGCTTCCAAAGCAGCGACATCGGCCAGCGTAGGTGGTCTTTGTCCCGGGA 120
Db 251 GCGTACCCGCTTCCAAAGCAGCGACATCGGCCAGCGTAGGTGGTCTTTGTCCCGGGA 192
QY 121 AAGACGGTTTCCAGAAATCCCGCGCGCGAGATGAACAGGACGATTCGTCTAACGTGCGC 180
Db 191 AAGACGGTTTCCAGAAATCCCGCGCGCGAGATGAACAGGACGATTCGTCTAACGTGCGC 132
QY 181 GAGGACTCGGTATCGTCAAGTTCCGTCGTCGAGCGAACGTTGTGGCGGCGTAATTGT 240
Db 131 GAGGACTCGGTATCGTCAAGTTCCGTCGTCGAGCGAACGTTGTGGCGGCGTAATTGT 72
QY 241 ACGCGCGCGCGAAATGTTCCGTGCGCATCATCTGTTAGCCCTTCGGCTGCTCTGGG 300
Db 71 ACGCGCGCGCGAAATGTTCCGTGCGCATCATCTGTTAGCCCTTCGGCTGCTCTGGG 12
QY 301 TTTGTCGACAT 311
Db 11 TTTGTCGACAT 1
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RESULT 4

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US-11-205-109-1/c
; Sequence 1, Application US/11205109
; Publication No. US20050287641A1
; GENERAL INFORMATION:
; APPLICANT: Farnet, Chris
; APPLICANT: Zazopoulos, Emmanuel
; APPLICANT: Staffa, Alfredo
; TITLE OF INVENTION: GENE CLUSTER FOR RAMOPLANIN BIOSYNTHESIS
; FILE REFERENCE: 3002-2US
; CURRENT APPLICATION NUMBER: US/11/205,109
; CURRENT FILING DATE: 2005-08-17
; PRIOR APPLICATION NUMBER: US/09/976,059
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US 60/239,924
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 88421
; TYPE: DNA
; ORGANISM: Actinoplanes sp.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2077)..(3078)
; OTHER INFORMATION: ORF 1; positive strandedness
```

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,
,
, NAME/KEY: misc feature
, LOCATION: (3118)..(4032)
, OTHER INFORMATION: ORF 2; positive strandedness
, FEATURE:
, NAME/KEY: misc feature
, LOCATION: (4038)..(5048)
, OTHER INFORMATION: ORF 3; positive strandedness
, FEATURE:
, NAME/KEY: misc feature
, LOCATION: (6665)..(5814)
, OTHER INFORMATION: ORF 4; negative strandedness
, FEATURE:
, NAME/KEY: misc feature
, LOCATION: (7703)..(6693)
, OTHER INFORMATION: ORF 5; negative strandedness
, FEATURE:
, NAME/KEY: misc feature
, LOCATION: (9464)..(8130)
, OTHER INFORMATION: ORF 6; negative strandedness
, FEATURE:
, NAME/KEY: misc feature
, LOCATION: (9691)..(10761)
, OTHER INFORMATION: ORF 7; positive strandedness
, FEATURE:
, NAME/KEY: misc feature
, LOCATION: (12751)..(10829)
, OTHER INFORMATION: ORF 8; negative strandedness
, FEATURE:
, NAME/KEY: misc feature
, LOCATION: (13617)..(12802)
, OTHER INFORMATION: ORF 9; negative strandedness
, FEATURE:
, NAME/KEY: misc feature
, LOCATION: (15203)..(13614)
, OTHER INFORMATION: ORF 10; negative strandedness
, FEATURE:
, NAME/KEY: misc feature
, LOCATION: (15591)..(15863)
, OTHER INFORMATION: ORF 11; positive strandedness
, FEATURE:
, NAME/KEY: misc feature
, LOCATION: (15850)..(19035)
, OTHER INFORMATION: ORF 12; positive strandedness
, FEATURE:
, NAME/KEY: misc feature
, LOCATION: (19032)..(39713)
, OTHER INFORMATION: ORF 13; positive strandedness
, FEATURE:
, NAME/KEY: misc feature
, LOCATION: (39713)..(65800)
, OTHER INFORMATION: ORF 14; positive strandedness
, FEATURE:
, NAME/KEY: misc feature
, LOCATION: (65826)..(68530)
, OTHER INFORMATION: ORF 15; positive strandedness
, FEATURE:
, NAME/KEY: misc feature
, LOCATION: (66546)..(67370)
, OTHER INFORMATION: ORF 16; positive strandedness
, FEATURE:
, NAME/KEY: misc feature
, LOCATION: (67384)..(70059)
, OTHER INFORMATION: ORF 17; positive strandedness
, FEATURE:
, NAME/KEY: misc feature
, LOCATION: (70059)..(70662)
, OTHER INFORMATION: ORF 18; positive strandedness
, FEATURE:
, NAME/KEY: misc feature
, LOCATION: (70659)..(71906)
, OTHER INFORMATION: ORF 19; positive strandedness
, FEATURE:
,
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, NAME/KEY: misc feature
, LOCATION: (73439)..(71964)
, OTHER INFORMATION: ORF 20; negative strandedness
, FEATURE:
, NAME/KEY: misc feature
, LOCATION: (74216)..(73563)
, OTHER INFORMATION: ORF 21; negative strandedness
, FEATURE:
, NAME/KEY: misc feature
, LOCATION: (75424)..(74213)
, OTHER INFORMATION: ORF 22; negative strandedness
, FEATURE:
, NAME/KEY: misc feature
, LOCATION: (75535)..(76464)
, OTHER INFORMATION: ORF 23; positive strandedness
, FEATURE:
, NAME/KEY: misc feature
, LOCATION: (78110)..(76449)
, OTHER INFORMATION: ORF 24; negative strandedness
, FEATURE:
, NAME/KEY: misc feature
, LOCATION: (79864)..(78107)
, OTHER INFORMATION: ORF 25; negative strandedness
, FEATURE:
, NAME/KEY: misc feature
, LOCATION: (81624)..(79861)
, OTHER INFORMATION: ORF 26; negative strandedness
, FEATURE:
, NAME/KEY: misc feature
, LOCATION: (81909)..(81682)
, OTHER INFORMATION: ORF 27; negative strandedness
, FEATURE:
, NAME/KEY: misc feature
, LOCATION: (82346)..(82062)
, OTHER INFORMATION: ORF 28; negative strandedness
, FEATURE:
, NAME/KEY: misc feature
, LOCATION: (82587)..(84446)
, OTHER INFORMATION: ORF 29; positive strandedness
, FEATURE:
, NAME/KEY: misc feature
, LOCATION: (84481)..(85548)
, OTHER INFORMATION: ORF 30; positive strandedness
, FEATURE:
, NAME/KEY: misc feature
, LOCATION: (85556)..(86845)
, OTHER INFORMATION: ORF 31; positive strandedness
, FEATURE:
, NAME/KEY: misc feature
, LOCATION: (87372)..(86803)
, OTHER INFORMATION: ORF 32; negative strandedness
, FEATURE:
, NAME/KEY: misc feature
, LOCATION: (87494)..(88420)
, OTHER INFORMATION: ORF 33; positive strandedness; N-terminus only
, US-11-205-109-1
```

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Query Match      3.7%; Score 57.4; DB 12; Length 88421;
Best Local Similarity 43.4%; Pred. No. 2.6e-05;
Matches 262; Conservative 0; Mismatches 341; Indels 0; Gaps 0;

QY 673 GCCACATGCTTGGCGTGGCGGATACACGGCCATGTTGTCGGGCACATGGCGATGT 732
    |||||
DB 40820 GCCCGAGGGCGGGACCGCGCGCGCATCAGGTCTCGGTCTCCACGGCAGCG 40761
    |||||

QY 733 CGCCATGCACCGGTGCGGAGTGCAGATACAGTCCAGGGGCGATGACGTCCGGCAGGAA 792
    |||||
DB 40760 CCACCTGGAACAGCGGTGCGGCTCAGCAGCCGACGCGGAGCTCTCTGACGAGCT 40701
    |||||

QY 793 TGTGCTGCTAGCGCTCGAGGCGACCGGTACACGGCCGAGTTGGTCTCGATGAAGTTCA 852
    |||||
DB 40700 TCTCGAAGCGGCACGCTCTGTTGGCCGCTACGCTCGAGGGCCCGCTCGCGGACCTCGCGCA 40641
    |||||
```

QY 853 AGATCAACGCGATCCAGGCTCAAGTTGCCCGCCACCCGAAACCGGGGGAACTTCGAGTCCT 912
Db 40640 GCAGGTCGCGAAGGTCGGGTCGCGGTCAGGTCGGCGCCGATCACCAAGTTGTTGAAGA 40581
QY 913 TGGCATGGCGGCTCTCCATATACCTCGGAGGGGATGGAAGCACACCGTCGCTTTGGGGT 972
Db 40580 AGCAGCGGACGAGTCTGTCAGGCGCGGCTGCGGTGCGCGCGGACACACCGTCGCGATCG 40521
QY 973 GCGGTCGAGGAATGCGACCTGTTTGTAGCTTCAGCGGATCGATCAGTAGTCGTCCG 1032
Db 40520 GCAGGTCGTCGCGCGCCCGAGCCGGAAGACCATGCGGTCGCGCGTGACGCGCCA 40461
QY 1033 CTTGCGCAACGCGAGCTACTTCGCGGAGCGGCGGACGAGCGGCGGTCAGGTTCCCAT 1092
Db 40460 TGAAGAGCGTGGCGCGAGCTCGCGGTGAGGGCGGTTCAGTCCGTCGGCGCGCG 40401
QY 1093 TGAGGCGGAGTTTTCGCTCTGAAGATCGCGCGGAACACGTCGGGGTACCGTCGCGGT 1152
Db 40400 GCACGCGGAATCGGCCATGTGCGCGCGGACGACGACGCGGCGGCGCGGTGCGG 40341
QY 1153 ACTCAGCGATGATCGCGGCGGTGCGATCGGTTCGACGCGGTGTCGGCGAGCATCTCCA 1212
Db 40340 CCGCAGCGCGAGCTCTCGGGGCTCCGCGAGCGCGGACCGCCAAATAGCCAGCTGCT 40281
QY 1213 CCGGGAAGTCGTTTGTCTGTCGAGAAAGCTGTCGAAGGCTGACGCGGCGTAGCCGCGCT 1272
Db 40280 CGCGCAGGAGCTCTCGGCTGTCACCGCGCGCGAGCACTCTCTGTCGACAGCGGT 40221
QY 1273 GGT 1275
Db 40220 AGT 40218

RESULT 5

US-11-143-401-127/c
; Sequence 127, Application US/11143401
; Publication No. US2006002953A1
; GENERAL INFORMATION:
; APPLICANT: Behr, Marcel
; APPLICANT: Small, Peter
; APPLICANT: Schoolnik, Gary
; APPLICANT: Wilson, Michael A.
; TITLE OF INVENTION: Molecular Differences Between Species of
; FILE REFERENCE: STAN102CON
; CURRENT APPLICATION NUMBER: US/11/143,401
; PRIOR FILING DATE: 2005-06-01
; PRIOR FILING DATE: US/10/647,089
; PRIOR FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: US/09/894,844
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/318,191
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 60/097,936
; PRIOR FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 127
; LENGTH: 1236
; TYPE: DNA
; ORGANISM: Mycobacteria tuberculosis
US-11-143-401-127

Query Match 3.7%; Score 56; DB 12; Length 1236;
Best Local Similarity 63.2%; Pred. No. 5.1e-05;
Matches 86; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
QY 1348 CGCAAGGTTATTCGATGGGAGAGTCAATCGCTGTGCGCGCGCGCGCTCGCGCTGCT 1407
Db 1062 CGGTGGGTTGATAGTCGCGCGCTCGATCGCGCTACCGAGGCTACCCAGAACCGC 1003
QY 1408 GGCCTGTGTGCGCGGACCTAGCGACAGCTGGCGAGTATAGCGAGGTGCACTGAC 1467

Db 1002 GGCCTTTGTGTCGGCGAGCTGTCAGCAAGCGCTCGCGAAACAGACGCGCAACATTTGGC 943
QY 1468 GTTGGGCTCGAACC GC 1483
Db 942 GTTGTCTCTGGAACGC 927
RESULT 6
US-11-122-329-122/c
; Sequence 122, Application US/11122329
; Publication No. US2006001927A1
; GENERAL INFORMATION:
; APPLICANT: Geraci, Mark
; APPLICANT: Bull, Todd
; APPLICANT: Voelkel, Norbert
; APPLICANT: Coldren, Chris
; TITLE OF INVENTION: Diagnosis of Disease and Monitoring of Therapy Using Gene
; FILE REFERENCE: 2848-54
; CURRENT APPLICATION NUMBER: US/11/122,329
; PRIOR FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/568,129
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 122
; LENGTH: 2155
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-122-329-122

Query Match 3.5%; Score 53; DB 12; Length 2155;
Best Local Similarity 48.0%; Pred. No. 0.0003;
Matches 182; Conservative 0; Mismatches 195; Indels 2; Gaps 1;
QY 319 CTCGACAGCGCGTTCGAGCGCGGAGGCGCACACATCCACGACCCCTCGCGCTCGGC- 377
Db 1588 CTGCTCTGCGGTGGGAAGACGCGCGCGCCAGGCGCGCCACTCTCGCGCTCGGGGTGCA 1529
QY 378 -GTGCGCGCGGAGAGTTGCGGCACATGGGTCTTTAGCGCGCGCGCGCGGTGTCGCCCGCG 436
Db 1528 GAGCCCGTTGTCAGGTAGCGGTGACGTAGACAGCGCGCGCGCGCGCGCGCGCG 1469
QY 437 GTGCTGCGAGCGGATCGCGATCGCGGATGCGCGGATGCGGTCTTCGACGCGCGCG 496
Db 1468 CAGCCGAGGTCACCGGACGCTGCGGTGGGTGGGCGCGGTGTCGCTCGCGTA 1409
QY 497 GCGCCCTCTCGGCGCTTGAACGTTGCGGATCTGCGGAAGGATCCAGTCGCGCATGACGC 556
Db 1408 GATCAGCACCGCGCGCGCGCGCTCGCGCGCGCGCTGGGCGGTGGCGCGAG 1349
QY 557 GATGAGCTCTCGCGCGCGGCTCTCCCGGGAACAGGTGAGCATCGCTCAACGTCGC 616
Db 1348 GAGCGCCACCGTGTGTTGTCGTCAGGACGCGTCCGCGCTGCGACACTTCGCGCCAGAG 1289
QY 617 CGCATGCCCGGACCGCTCGGTCAACAGAACTTTGCGGCTCCACCACTGTTGTGCCA 676
Db 1288 CTGCTCTCATCCAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1229
QY 677 CATGCTTGGGCGTGGCGG 695
Db 1228 CTGACGTCGCGCGCGCGG 1210

RESULT 7

US-11-202-566-8/c
; Sequence 8, Application US/11202566
; Publication No. US20060029609A1
; GENERAL INFORMATION:
; APPLICANT: Zankel et al.
; TITLE OF INVENTION: USE OF THE CHAPERONE RECEPTOR-ASSOCIATED PROTEIN (RAP) FOR THE
; FILE REFERENCE: DELIVERY OF THERAPEUTIC COMPOUNDS TO THE BRAIN AND OTHER TISSUES
; FILE REFERENCE: 30610/39383

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; CURRENT APPLICATION NUMBER: US/11/202,566
; CURRENT FILING DATE: 2005-08-12
; PRIOR APPLICATION NUMBER: US/10/600,862
; PRIOR FILING DATE: 2003-06-20
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 2937
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: RAP-IDS fusion sequence
US-11-202-566-8

Query Match      3.5%; Score 53; DB 9; Length 2937;
Best Local Similarity 48.0%; Pred. No. 0.00031;
Matches 182; Conservative 0; Mismatches 195; Indels 2; Gaps 1;

QY 319 CTCGACAGCCGGTCGGAGCCGGAGGCCACACATCCACGAGCCCTCGCGGCTCGGC- 377
DB 2469 CTGCTCTGCCGTGGGGAAGACGGCGCCAGCGCCGCTCGCCCTCGCGGCTGCA 2410
QY 378 -GTCGCGGGCGGAGCTTCGCGCACTTGGGTCTTGGAGCCGCCCGCGGGTGTGCGCCCGCG 436
DB 2409 GAGCCCGTGTTCAGGTAGCGGTGACGTAGACAGGCCCGCGCGGGGGCACCCCGCG 2350
QY 437 GTGCTGACGCCAGCATCGGGGATCGGGGATGCGCGCGATGTTTCTGTCAGCGCGGC 496
DB 2349 CAGCGCGCAGGTCACCGCAGCGTGGGTGGGGTGGGGTGGGGTGTCTGCTCGCGGTA 2290
QY 497 GCGCCCTTCGGGCTTGGACGCTTGGCGATCTGGCGAAGATCCAGTCGGCCATGACGCG 556
DB 2289 GATCAGCACCGCGCGCGCGCAGCGCTCGCGCGGGCCCTGGCGGCTGGCGCTGCGCCAG 2230
QY 557 GATGAGCTCTCTCGCGCGCGGGTCTCCCGGGAAACAGGTCCAGCATCGCGTCAAAAGTCGC 616
DB 2229 GAGGCCACCGTGTGTTGCTGTCCAGGACGGTCCCGGCTCGGACACTTCGGCCAGAG 2170
QY 617 CGCATGCCCGGACCTCGGTCAACAGAACTTTGGCGGGTCCACCACTGTTGTGCGCA 676
DB 2169 CTGCTCTCATCCAGCAGCGCCAGCAGCCCATGCGCGGTGAGCAGCGGCTTGGCAACAG 2110
QY 677 CATGCTTGGCGGTGCGG 695
DB 2109 CTGCACGTGCGCGGCGG 2091

RESULT 8
US-10-895-011-1/c
; Sequence 1, Application US/10895011
; Publication No. US20050281804A1
; GENERAL INFORMATION:
; APPLICANT: KAKKIS, EMIL D.
; TITLE OF INVENTION: METHODS FOR TREATING DISEASES CAUSED BY DEFICIENCIES OF
; FILE REFERENCE: 008000051CNUS01
; CURRENT APPLICATION NUMBER: US/10/895,011
; CURRENT FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: US/09/993,241
; PRIOR FILING DATE: 2001-11-13
; PRIOR FILING DATE: 2000-11-09
; PRIOR FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 6200
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1558)...(3510)
US-11-038-372-1

Query Match      3.5%; Score 53; DB 12; Length 6200;
Best Local Similarity 48.0%; Pred. No. 0.00032;
Matches 182; Conservative 0; Mismatches 195; Indels 2; Gaps 1;

QY 319 CTCGACAGCCGGTCGGAGCCGGAGGCCACACATCCACGAGCCCTCGCGGCTCGGC- 377
DB 3051 CTGCTCTGCCGTGGGGAAGACGGCGCCAGCGCCGCTCGCCCTCGCGGCTGCA 2992
QY 378 -GTCGCGGGCGGAGCTTCGCGCACTTGGGTCTTGGAGCCGCCCGCGGGTGTGCGCCCGCG 436
DB 2991 GAGCCCGTGTTCAGGTAGCGGTGACGTAGACAGGCCCGCGGGGGCACCCCGCG 2932
QY 437 GTGCTGACGCCAGCATCGGGGATCGGGGATGCGCGCGATGTTTCTGTCAGCGCGGC 496
DB 2931 CAGCGCGCAGGTCACCGCAGCGTGGGTGGGGTGGGGTGGGGTGTCTGCTCGCTCGCGTA 2872
QY 497 GCGCCCTTCGGGCTTGGACGCTTGGCGATCTGGCGAAGATCCAGTCGGCCATGACGCG 556
DB 2871 GATCAGCACCGCGCGCGCGCAGCGCTCGCGCGGGCCCTGGGGGCGGTGGCGCTGGCCAG 2812
QY 557 GATGAGCTCTCTCGCGCGCGGGTCTCCCGGGAAACAGGTCCAGCATCGCGTCAAAAGTCGC 616
DB 2811 GAGGCCACCGTGTGTTGCTGTCCAGGACGGTCCCGGCTCGGACACTTCGGCCAGAG 2752
QY 617 CGCATGCCCGGACCTCGGTCAACAGAACTTTGGCGGGTCCACCACTGTTGTGCGCA 676
DB 2751 CTGCTCTCATCCAGCAGCGCCAGCAGCCCATGCGCGGTGAGCAGCGGCTTGGCAACAG 2692
QY 677 CATGCTTGGCGGTGCGG 695
DB 2691 CTGCACGTGCGCGGCGG 2673

RESULT 9
US-11-038-372-1/c
; Sequence 1, Application US/11038372
; Publication No. US20050260185A1
; GENERAL INFORMATION:
; APPLICANT: KAKKIS, EMIL D.
; TITLE OF INVENTION: METHODS FOR TREATING DISEASES CAUSED BY DEFICIENCIES OF
; FILE REFERENCE: 008000051CNUS01
; CURRENT APPLICATION NUMBER: US/11/038,372
; CURRENT FILING DATE: 2005-01-18
; PRIOR APPLICATION NUMBER: US/10/895,011
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: US/09/993,241
; PRIOR FILING DATE: 2001-11-13
; PRIOR FILING DATE: 09/711,205
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 09/439,923
; PRIOR FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 6200
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1558)...(3510)
US-11-038-372-1

Query Match      3.5%; Score 53; DB 12; Length 6200;
Best Local Similarity 48.0%; Pred. No. 0.00032;
Matches 182; Conservative 0; Mismatches 195; Indels 2; Gaps 1;

QY 319 CTCGACAGCCGGTCGGAGCCGGAGGCCACACATCCACGAGCCCTCGCGGCTCGGC- 377
DB 3051 CTGCTCTGCCGTGGGGAAGACGGCGCCAGCGCCGCTCGCCCTCGCGGCTGCA 2992
```

QY 378 -GTCCGGCGCGAGCTTCCGCCACTGGGTCTTGGAGCCGCGCGGGGTCTCGCCCCGCG 436
Db 2991 GAGCCCGTTTCCAGGTAGCGGTAGACAGAGCCCGGCGCGGCGCACCCCGCG 2932
QY 437 GTCTCGAGCGCAGCATGCGGATCCGGGATGCGCGGATGTTCTCGACGCGCGC 496
Db 2931 CAGCCGAGGGTCAACCGCAGCTGCGGTGGGGTGGCGCGGGTGTCTGCTCGCGTA 2872
QY 497 GCGCCCTCCGCGCTTGGAGCTTGGGATCTCGGCAAGGATCCAGTTCGGCCATGACGC 556
Db 2871 GATCAGACCGCGCGCGCAGCGGTGCGCGGCGCTTGGGCGGTGGCGGTGCGCAG 2812
QY 557 GATGAGCTCTCCGCGCGCGGGTCTCCCGGGAACAGGTCCAGCATCGCGTCAAACTGCG 616
Db 2811 GAGCCCAACCGTGTGGTGTCTCCAGGACGGTCCCGGCTCGACACTTCGSCCCAGAG 2752
QY 617 CGATGCGCGGACCTCGCTGAACAGAACTTTGGCGGGTCCACACCTGTTGTGCGCA 676
Db 2751 CTGCTCTCATCCAGCAGCGCCAGCAGCCCATGGCGGTGAGCACCGGCTTGGCAACAG 2692
QY 677 CATGCTTGGCGGTGCGG 695
Db 2691 CTGCACGTGCGCGCGG 2673

RESULT 10

US-10-522-037-1
; Sequence 1, Application US/10522037
; Publication No. US20050282166A1
; GENERAL INFORMATION:
; APPLICANT: LIBRAGEN
; TITLE OF INVENTION: Method for the expression of unknown environmental DNA into adapt
; FILE OF INVENTION: cells.
; FILE REFERENCE: B0149W0
; CURRENT APPLICATION NUMBER: US/10/522,037
; CURRENT FILING DATE: 2005-01-24
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 37500
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: DNA sequence of clone FS3-124.
US-10-522-037-1

Query Match 3.5%; Score 53; DB 8; Length 37500;
Best Local Similarity 46.5%; Pred. No. 0.00034;
Matches 259; Conservative 0; Mismatches 280; Indels 18; Gaps 2;

QY 672 TGCACATGCTTGGCGGTGGCGGATACACGGCCATGGTTCGGGGCAACATGGCGATG 731
Db 17958 TTCGACATGTTGGTGTGTCGACGCTGTATGCGTCAGGGGTTCGGGATGAACCGACC 18017
QY 732 TCGCCATGACCCGCTGCGGAGCTGCAGATACAGTCCAGGGGATGACGTCCGGCAGGA 791
Db 18018 GGGCCCTTCGCCAGAGGCGCAGCAGAGTCCAGATCTCTGACGCGGTGGATCCGGTTC 18077
QY 792 ATGTCTGCTGAGCGCTCGAGGGACCGGTATACGCGCCAGTTGGTCTGGATGAAGTTTCATC 851
Db 18078 GCGAACATCTCTCGCGGAGCAGCGCGGCTTTGACCATGACCGGATGCGGCG 18137
QY 852 AAGATCAACGCATCCAGGTCAAGTTGCCCCGACCCGACCGGGGGGAATCTCGAGTCC 911
Db 18138 TTTTCGAGGACGAGGTTCGGGAGACAGCGCCCTTCGAGCGCGCGGAAGATCGAGCGTGC 18197
QY 912 TTGGCATGGCGCTCTCCCATATCACTTCGAGCGGGATGGAAGCACACCGCTGCTTGGGG 971
Db 18198 AGACCTCGCGCGCTCTGTCGATGAGCGCGCGCGCTATGATGAAGTCCAGTCCGGCG 18257
QY 972 TCGCGGTTCGAGGAATCGACCTGTTTGTTCAGTTCAGCGGATTCAGTAGTCTGCTCC 1031
Db 18258 TGCTGTGCGAAGAGATCGACCTGCGCGGGAATCTTGGCGCGATC---CCACGAGTCTGTCG 18314

QY 1032 GCTCGCACACAGCGCAGCTACTCGCGCGAGCGGCGCAGCGCGCTCAGGTTTCCCA 1091
Db 18315 GGTTCGAGCAGCGCACAGATTTCCCTCTCGCGCGCGCGATGGCGGATTCGGGCGCGC 18374
QY 1092 TTGAGCGCGAGGTTTTCGCTCTGAAGATCGGCGCGGAAACACGTGCGGGTACCGCTCGGG 1151
Db 18375 GCAAGCGCGGCTTGGC-----CTGAGAGATCACCGTATGATGGCGCGCGC 18419
QY 1152 TACTCAGCATGATCGCGGGTGGCATCGTTCGAGCGCTCGTTCGCGCAGCATGATCTCC 1211
Db 18420 AATCTCGCAGGATGTCTCCCTGCGCTCGGTCTCGATTCCTGTCGACGACGATCACTTCG 18479
QY 1212 ACCGGGAAGTCCGTTTG 1228
Db 18480 ACGGCTGATAGTCTG 18496

RESULT 11

US-10-858-730-133/c
; Sequence 133, Application US/10858730
; Publication No. US20050255568A1
; GENERAL INFORMATION:
; APPLICANT: Bailey, Richard B.
; APPLICANT: Blomquist, Paul
; APPLICANT: Doten, Reed
; APPLICANT: Driggers, Edward M.
; APPLICANT: Madden, Kevin T.
; APPLICANT: O'Leary, Jessica
; APPLICANT: O'Toole, George
; APPLICANT: Trueheart, Joshua
; APPLICANT: Walbridge, Michael J.
; APPLICANT: Yorgey, Peter S.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR AMINO ACID
; FILE OF INVENTION: PRODUCTION
; FILE REFERENCE: 14184-030001
; CURRENT APPLICATION NUMBER: US/10/858,730
; CURRENT FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/475,000
; PRIOR FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: US 60/551,860
; PRIOR FILING DATE: 2004-03-10
; NUMBER OF SEQ ID NOS: 364
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 133
; LENGTH: 1386
; TYPE: DNA
; ORGANISM: Streptomyces coelicolor
US-10-858-730-133

Query Match 3.2%; Score 49.6; DB 8; Length 1386;
Best Local Similarity 44.0%; Pred. No. 0.0022;
Matches 263; Conservative 0; Mismatches 329; Indels 6; Gaps 1;

QY 682 CTTGGCGGTGGCGGATACACGGCCATGGTTCGGGGCAACATGGCGATGTCGCCATGCA 741
Db 916 CGTCAGCGCGCGCGCTCGACTCTCTTGATCTGTTGAGCAGGTGAGGTGATGCCCT 857
QY 742 CCGCTGCGCGACGTGTCAGATACCATCCAGTCCAGGGGATGACGTCCGCGAGAAATGTCGT 801
Db 856 TCTCGTCGACGACGTAGCCGAGGAGTCCGAGCGGTGACCGGCTTGGCGCGCGGCGG 797
QY 802 AGCGTTCGAGGCGACGGTACACGGCCGATTTGGTCTGGATGAGTTTCATCATAGATCAACG 861
Db 796 TCAGCTTCTCGATGTTGATGTCGCCACGTTGCCGAGCCGAGAGCAGCCGCGGTCTGGC 737
QY 862 CATTCAGGCTCAAGTTGCCCGCCACCCGAAACCGGGGGAACTTTCGAGTCTTTGGCATGGC 921
Db 736 CTTCCAGGTCTTCGCGCGCTCCGCGCATCGCGCGCGCAACAGCAGTTCGCCGTAGC 677
QY 922 CFTCTCTCCATATCACTCGGACGGGATGGAAGACACACCTGTCGTTGGGGTTCGCGTCA 981
Db 676 CGGTCTGCTCCGGGGGATCAGCGAGCCCGCCAGCCCTTGGCCCTTGGCGGTTCAGGACGC 617

QY 982 GGAATCGACCTGTTGCTTAGCTTCAGCGGATCGATCCAGTAGTCTGTCGGCTCGCACA 1041
Db 616 CGGACTCCAGCGGTGGTGATCCGCCGTACTGGCCGAAGAGGTAGCCGATCTCGCGGC 557
QY 1042 AGCGACGTACTCGCCGCGAGCGCCGACAGAGCGCGGTCAAGTTTCCCATTTGAGGCCGA 1101
Db 556 CCCCCA-----CGCGATGTCCCGCGCGGACGTCCTGTGCTCGCGATGTGCCGT 503
QY 1102 GGTTCGCTCTGAAGATCGGCGGAAACAGTGGGGTACCGCTCGCGGTACTCACGGA 1161
Db 502 ACAGCTCCGTCATGAAGACTGCGAGAACCGCATGACCTCCGCGTCGCTGCGCCGTGCG 443
QY 1162 TGATCGCGGGTGGCATCGGTGCGCGCTGTGCGGACGATGATCTCCACCGGGAAGT 1221
Db 442 GGTGGAAGTCGCTGCCGCCCTTTGCCGCCCGCATGCCGAGCGCGGTACGCGGTCTTGA 383
QY 1222 CGGTTTGTGTCGAGAAAGCTGTGCAAGGCTTGACGGCGGTAGCCGCGCTGTTGTG 1279
Db 382 AGATCTGCTCGAAGCCAGGAATTGATGACGCCAGGTTGACGGAAGGATGGAAGCG 325

RESULT 12

US-11-075-185-35/c

; Sequence 35, Application US/11075185
; Publication No. US20050266434A1

GENERAL INFORMATION:

; APPLICANT: REEVES, CHRISTOPHER D

; APPLICANT: JULIEN, BRYAN

; APPLICANT: REID, RALPH

; TITLE OF INVENTION: BIOSYNTHETIC GENE CLUSTER FOR AMBRUTICINS

; CURRENT APPLICATION NUMBER: US/11/075,185

; CURRENT FILING DATE: 2005-03-07

; PRIOR APPLICATION NUMBER: US 60/551,103

; PRIOR FILING DATE: 2004-03-08

; PRIOR APPLICATION NUMBER: US 60/568,290

; PRIOR FILING DATE: 2004-05-04

; NUMBER OF SEQ ID NOS: 61

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 35

; LENGTH: 10968

; TYPE: DNA

; ORGANISM: Sorangium cellulosum

US-11-075-185-35

Query Match 3.1%; Score 47.2; DB 12; Length 10968;
Best Local Similarity 45.8%; Pred. No. 0.01;
Matches 163; Conservative 0; Mismatches 193; Indels 0; Gaps 0;

QY 335 GAGCCGGGAGGGCCACATCCACAGAGCCCTCTGCGGCTCGCGGCGCGGAGCTT 394
Db 9039 GCGCTCGCTCGGCGCGCGAGCGCGCACCCGCTCCGTGCTCGCGCGGCTGGAA 8980
QY 395 GCGCCACTCGGTCTTGAGCGCGCGCGGCTGTCGCCCGCGGTCTGCAGCGCCAGCAT 454
Db 8979 CGCCCCACCGCGCGACCGCGCGCCCTCGCGGTTCGGGAGGTGATCGACCGCTGAG 8920
QY 455 GCGCGATCCGGGATGCGCGCGATGTTTCTTCAGCGCGCGCGCCCTCCGGGCTGG 514
Db 8919 CCCCTCCCGTCTCTCCGCGCTCTGTTTTCAGGGGACGCGCACCTCCGCTGCCCGCG 8860
QY 515 AACGTTGGCGATCTGGCGAAGATCCAGTCGCGCATGACGGGATGAGCTCTTCGGCGC 574
Db 8859 CGCCTCGATCAGCAGCTCCGAGAACCGAACCGCAGCAGCATCTTGTCTGCTCGGACGC 8800
QY 575 GGGGTCTCCGGGACAGTTCGAGCATCGGTCAACAGCTCGCGCATGCCCGGACCTCG 634
Db 8799 CTCCTCTCGCGCGACCGCGCAGCAACGAGTGCAGACCTGTTGTGCCACATGCCCTTGGCGGT 8740
QY 635 CGTCAACAGAACTTTGGCGGGTCCACCACTGTTGTGCCACATGCCCTTGGCGGT 690
Db 8739 GATCCGGAAGCTCTGCGCGGTGTCGCCACCGCTCCGGCAGCGGACCCGCGGT 8684

RESULT 13

US-11-075-185-1/c

; Sequence 1, Application US/11075185
; Publication No. US20050266434A1

GENERAL INFORMATION:

; APPLICANT: REEVES, CHRISTOPHER D

; APPLICANT: JULIEN, BRYAN

; APPLICANT: REID, RALPH

; TITLE OF INVENTION: BIOSYNTHETIC GENE CLUSTER FOR AMBRUTICINS

; FILE REFERENCE: 010099.03

; CURRENT APPLICATION NUMBER: US/11/075,185

; CURRENT FILING DATE: 2005-03-07

; PRIOR APPLICATION NUMBER: US 60/551,103

; PRIOR FILING DATE: 2004-03-08

; PRIOR APPLICATION NUMBER: US 60/568,290

; PRIOR FILING DATE: 2004-05-04

; NUMBER OF SEQ ID NOS: 61

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 1

; LENGTH: 78869

; TYPE: DNA

; ORGANISM: Sorangium cellulosum

US-11-075-185-1

Query Match 3.1%; Score 47.2; DB 12; Length 78869;
Best Local Similarity 45.8%; Pred. No. 0.011;
Matches 163; Conservative 0; Mismatches 193; Indels 0; Gaps 0;

QY 335 GAGCCGGGAGGGCCACATCCACAGAGCCCTCTGAGCGCGCGGCTGTCGCCCGCGGTCTGCAGCGCCAGCAT 454
Db 24306 GCGCTCGTTCGCGCGCGCGAGCGCGCACCCGCTCCGTGCTCGCGCGCTGGAA 24247
QY 395 GCGCCACTCGGTCTTGAGCGCGCGCGGCTGTCGCCCGCGGTCTGCAGCGCCAGCAT 454
Db 24246 CGCCCCACCGCGCGAGCGCGCGCCCTCGCGGTTCGGGAGGTGATCGACCGCTGAG 24187
QY 455 GCGGATCCGGGATGCGCGCGATGTTTCTTCAGCGCGCGCGCCCTTCGGGCTTGG 514
Db 24186 CCCCTCCCGTCTCTCCGCGCTCTGTTTTCAGGCGGAGCGCACCTCCGCTGCCCGCG 24127
QY 515 AACGTTGGCGATCTCGCGAAGATCCAGTCGCGCATGACGGGATGAGCTCTTCGCGCGC 574
Db 24126 CGCCTCGATCAGCAGCTCGAGAACCGAACCGCAGCAGCATCTTGTCTGCTCGGACGC 24067
QY 575 GGGGTCTCCGGGAAACAGTTCGAGCATCGCGTCAACAGCTCGCGCATGCCCGGACCTCG 634
Db 24066 CTCCTCTTCGCGCGACCGCGCCAGCAACGAGTGCAGCACCGCGTTCGAGCAGCGCGATG 24007
QY 635 CGTCAACAGAACTTTGGCGGGTCCACCACTGTTGTGCCACATGCCCTTGGCGGT 690
Db 24006 GATCCGGAAGCTCTGCGCGGTGTCGCCACCGCTCCGGCAGCGGACCCGCGGT 23951

RESULT 14

US-11-024-959-78/c

; Sequence 78, Application US/11024959
; Publication No. US20060010516A1

GENERAL INFORMATION:

; APPLICANT: FORSTER, RICHARD L.

; APPLICANT: CONNETT, MARIE B.

; APPLICANT: EMERSON, SARAH JANE

; APPLICANT: GRIGOR, MURRAY ROBERT

; APPLICANT: HIGGINS, COLLEEN M.

; APPLICANT: LUND, STEVEN TROY

; APPLICANT: MAGUSIN, ANDREAS

; APPLICANT: KODRZYCKI, BOB

; TITLE OF INVENTION: CELL CYCLE GENES AND RELATED METHODS

; FILE REFERENCE: 044463-0360

; CURRENT APPLICATION NUMBER: US/11/024,959

; CURRENT FILING DATE: 2004-12-30

; PRIOR APPLICATION NUMBER: 60/533,036

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QY 301 CGGGGAGACGTCGATCGCGGTGTAATCAGTTTGAAGCCACGCGCATCTAGTAGTCCA 360
Db 301 CGGGGAGACGTCGATCGCGGTGTAATCAGTTTGAAGCCACGCGCATCTAGTAGTCCA 360
QY 361 GTAGAGCCCCATAGCCACACGCTTAGATCGTTCGAAAAATGGTCCGCCGCAATTGACAA 420
Db 361 GTAGAGCCCCATAGCCACACGCTTAGATCGTTCGAAAAATGGTCCGCCGCAATTGACAA 420
QY 421 TCGGCACACAGCTGGTCAAAAGCGCAACGCTCGCCCGCTTCGCGTTCCAAATCGACGCCG 480
Db 421 TCGGCACACAGCTGGTCAAAAGCGCAACGCTCGCCCGCTTCGCGTTCCAAATCGACGCCG 480
QY 481 GGGGTGCGCTGCTTCGAGTTTCGATCGGTAGTAACGGGCCACGTCAGCGAGCATGCT 540
Db 481 GGGGTGCGCTGCTTCGAGTTTCGATCGGTAGTAACGGGCCACGTCAGCGAGCATGCT 540
QY 541 CGTTGCGTCTTCGCCCATGAAGCTGCTCAGATTGCTGTGTGGGCGTCCGTCGCTGG 600
Db 541 CGTTGCGTCTTCGCCCATGAAGCTGCTCAGATTGCTGTGTGGGCGTCCGTCGCTGG 600
QY 601 GTCCGAGACTATACCTTCAACAGTTGCATGCGAGGCTCGCGGGGCAATGACCCAAAA 660
Db 601 GTCCGAGACTATACCTTCAACAGTTGCATGCGAGGCTCGCGGGGCAATGACCCAAAA 660
QY 661 CCGCGCGGACGCTTCGCGGACGCAAGAGCGTGGAGACGATAGATAATTTCACTGGCGA 720
Db 661 CCGCGCGGACGCTTCGCGGACGCAAGAGCGTGGAGACGATAGATAATTTCACTGGCGA 720
QY 721 CAGTACTCTCAAATAGTCCGGAGCCTCGGCTCCGACGTTAAAGAGCAGATCCAGATCCGAC 780
Db 721 CAGTACTCTCAAATAGTCCGGAGCCTCGGCTCCGACGTTAAAGAGCAGATCCAGATCCGAC 780
QY 781 ACGCGGGCTCGAACCCCTCCCACAATTCGTTATATATCGCGGTAGCCGTCATAATCGAAC 840
Db 781 ACGCGGGCTCGAACCCCTCCCACAATTCGTTATATATCGCGGTAGCCGTCATAATCGAAC 840
QY 841 CAAGTTACCCGGATGCTAAGTTGCTCGAACACGCGCTCATCGACATACCAACGGGCTGAG 900
Db 841 CAAGTTACCCGGATGCTAAGTTGCTCGAACACGCGCTCATCGACATACCAACGGGCTGAG 900
QY 901 GGGCCAGAGACATATTCGGTTCGCTCGCGGCTGTGGCAGAGGTTGGCCAGTCTCTCGGTC 960
Db 901 GGGCCAGAGACATATTCGGTTCGCTCGCGGCTGTGGCAGAGGTTGGCCAGTCTCTCGGTC 960
QY 961 TTGCGCTCGGCTAAATTCGTAGTCCCAAGAAATTTGCCAGTTCGTGATACCGAGATAA 1020
Db 961 TTGCGCTCGGCTAAATTCGTAGTCCCAAGAAATTTGCCAGTTCGTGATACCGAGATAA 1020
QY 1021 CTGCAATCGCATTCGAATAGCCGTTGAGTTAGGAAAGATTTCGTGCTGTTCTTCG 1080
Db 1021 CTGCAATCGCATTCGAATAGCCGTTGAGTTAGGAAAGATTTCGTGCTGTTCTTCG 1080
QY 1081 AGGTAATCGCGCGAGCCAGTCAGCGATCTCCGCAAAATGAGCGGCCGCGCTGTAGTTG 1140
Db 1081 AGGTAATCGCGCGAGCCAGTCAGCGATCTCCGCAAAATGAGCGGCCGCGCTGTAGTTG 1140
QY 1141 AATTCGTAGTCCGCGCAGTCGCGTTTCGCCCAATCGGTCCGTCGATCAGCGTCTCACGT 1200
Db 1141 AATTCGTAGTCCGCGCAGTCGCGTTTCGCCCAATCGGTCCGTCGATCAGCGTCTCACGT 1200
QY 1201 ATCTTTGATGAAAGCTCCCTTCACCTCGAGCGGGAAGATTATCCACTGTAACCCCTGG 1260
Db 1201 ATCTTTGATGAAAGCTCCCTTCACCTCGAGCGGGAAGATTATCCACTGTAACCCCTGG 1260
QY 1261 CTTCGTTTTCGATTCGATTCCTGTTTCGCCCAATCAGCGTTCGTTATTTGCAATCATATAG 1320
Db 1261 CTTCGTTTTCGATTCGATTCCTGTTTCGCCCAATCAGCGTTCGTTATTTGCAATCATATAG 1320
QY 1321 ATGATGAATTCATCGACGAATCGAATCAGGTCAAAATATCCTCGCAAGGTATGTAATTT 1380
Db 1321 ATGATGAATTCATCGACGAATCGAATCAGGTCAAAATATCCTCGCAAGGTATGTAATTT 1380
QY 1381 GATTGACAAATCGCGACTTCTTCAAC 1407
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Db 1381 GATTGACAAATCGCGACTTCTTCAAC 1407

RESULT 2

US-09-670-314-1
; Sequence 1, Application US/09670314
; Patent No. 6492506
; GENERAL INFORMATION:
; APPLICANT: Buchrieser-Brosch, Roland
; APPLICANT: Gordon, Stephen
; APPLICANT: Billault, Alain
; TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM
; TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA
; FILE REFERENCE: 3495-0169
; CURRENT APPLICATION NUMBER: US/09/670,314
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/060,756
; PRIOR FILING DATE: 1998-04-16
; NUMBER OF SEQ ID NOS: 743
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 12732
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-09-670-314-1

Query Match 100.0%; Score 1407; DB 3; Length 12732;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1407; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACCTCGCTTCGAGAGATCAAAATAGGCGGCATGGGTGAGCATAGTACAGGTGTCGCGCA 60
Db 1 ACCTCGCTTCGAGAGATCAAAATAGGCGGCATGGGTGAGCATAGTACAGGTGTCGCGCA 60
QY 61 TCTTTGATGATCGGAATAGATGTCAGGCAATTAAGAGAGAGCCAGCGGCTCGCG 120
Db 61 TCTTTGATGATCGGAATAGATGTCAGGCAATTAAGAGAGAGCCAGCGGCTCGCG 120
QY 121 CATTGAGCATGTCGAGCGTCGCTTCGATGAGCGCACCATTCCGCTGTCACAGATTCA 180
Db 121 CATTGAGCATGTCGAGCGTCGCTTCGATGAGCGCACCATTCCGCTGTCACAGATTCA 180
QY 181 GACGAACATTGAATATTCACCTCGCGACGCTATAGTCGCGCTCCGATCTATGCGCGCG 240
Db 181 GACGAACATTGAATATTCACCTCGCGACGCTATAGTCGCGCTCCGATCTATGCGCGCG 240
QY 241 CGCAGATGAAGTCTCGGTCGCGCAGCTTCGAAACGATAGTCGCGCGCGCGCACCATTT 300
Db 241 CGCAGATGAAGTCTCGGTCGCGCAGCTTCGAAACGATAGTCGCGCGCGCGCACCATTT 300
QY 301 CGGGGAGACGTCGATGCGGCTGTAATCAGTTTGAAGCCACGCGCATCTAGTAGTCCA 360
Db 301 CGGGGAGACGTCGATGCGGCTGTAATCAGTTTGAAGCCACGCGCATCTAGTAGTCCA 360
QY 361 GTAGAGCCCCATAGCCACACGCTTAGATCGTTCGAAAAATGGTCCGCCGCAATTGACAA 420
Db 361 GTAGAGCCCCATAGCCACACGCTTAGATCGTTCGAAAAATGGTCCGCCGCAATTGACAA 420
QY 421 TCGGCACACAGCTGGTCAAAAGCGCAACGCTCGCCCGCTTCGCGTTCCAAATCGACGCCG 480
Db 421 TCGGCACACAGCTGGTCAAAAGCGCAACGCTCGCCCGCTTCGCGTTCCAAATCGACGCCG 480
QY 481 GGGGTGCGCTGCTTCGAGTTTCGATCGGTAGTAACGGGCCACGTCAGCGAGCATGCT 540
Db 481 GGGGTGCGCTGCTTCGAGTTTCGATCGGTAGTAACGGGCCACGTCAGCGAGCATGCT 540
QY 541 CGTTGCGTCTTCGCCCATGAAGCTGCTCAGATTGCTGTGTGGGCGTCCGTCGCTGG 600
Db 541 CGTTGCGTCTTCGCCCATGAAGCTGCTCAGATTGCTGTGTGGGCGTCCGTCGCTGG 600

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QY 601 GTCCGAGACTATACCTTTCAACAGTTGTCATCCGAGGCTGCGCGGCAATGACCCAAAA 660
Db 601 GTCCGAGACTATACCTTTCAACAGTTGTCATCCGAGGCTGCGCGGCAATGACCCAAAA 660
QY 661 CCAGCGGACAGGTTCCGCGAGCAAGGAGCGTGGAGACATAGATAATTTCACTGCGCA 720
Db 661 CCAGCGGACAGGTTCCGCGAGCAAGGAGCGTGGAGACATAGATAATTTCACTGCGCA 720
QY 721 CAGTACCTCAAATAGTCCGAGGCTCGGCTCCGACGTTAAAGAGCAGATCCAGAATCGAC 780
Db 721 CAGTACCTCAAATAGTCCGAGGCTCGGCTCCGACGTTAAAGAGCAGATCCAGAATCGAC 780
QY 781 ACAGCGGCTCGAACCCTCCCAAAATGCTTAAATCGCGGTAGCGGTAGATTAATCGAAC 840
Db 781 ACAGCGGCTCGAACCCTCCCAAAATGCTTAAATCGCGGTAGCGGTAGATTAATCGAAC 840
QY 841 CAAGTTACCGGATGCTAGTTCGTCGAAACACGCGCTCATCGACATACGAAACGGGTGAG 900
Db 841 CAAGTTACCGGATGCTAGTTCGTCGAAACACGCGCTCATCGACATACGAAACGGGTGAG 900
QY 901 GGGCCAGAGACATATTCGGTTCGCGGCTGTTGGCAGAGGTTGGCCAGTCTCTCGGTC 960
Db 901 GGGCCAGAGACATATTCGGTTCGCGGCTGTTGGCAGAGGTTGGCCAGTCTCTCGGTC 960
QY 961 TTGCGGTCGCGTAAATTCGTAGTCCCAAGAAATTTGCCAGTTCGTGATACCGAGATAA 1020
Db 961 TTGCGGTCGCGTAAATTCGTAGTCCCAAGAAATTTGCCAGTTCGTGATACCGAGATAA 1020
QY 1021 CTCGAAATCGCATTCATAGACGCTGTTGAGTAAGAAAGATTCGTGTCGTTCTTCG 1080
Db 1021 CTCGAAATCGCATTCATAGACGCTGTTGAGTAAGAAAGATTCGTGTCGTTCTTCG 1080
QY 1081 AGGTAATCGCGCGAGCCAGTCAGCGATCTCCGCAAAATGAGCGCGCGCTGTAGTTG 1140
Db 1081 AGGTAATCGCGCGAGCCAGTCAGCGATCTCCGCAAAATGAGCGCGCGCTGTAGTTG 1140
QY 1141 AATTCGTAGTCCGCGCAGTCGCTTTTCGCCAATCGGTGCGGTCGATCAGCGTCTCACGT 1200
Db 1141 AATTCGTAGTCCGCGCAGTCGCTTTTCGCCAATCGGTGCGGTCGATCAGCGTCTCACGT 1200
QY 1201 ATCTTTGATGGAACGTCCTTCACCTGGAACGGAACGATTAACATCTGTAACCCCTGG 1260
Db 1201 ATCTTTGATGGAACGTCCTTCACCTGGAACGGAACGATTAACATCTGTAACCCCTGG 1260
QY 1261 CTCGTTTCATCCGATTCGTTTCGCAATCAGCTTCGTAATTCGATGTCATCATAG 1320
Db 1261 CTCGTTTCATCCGATTCGTTTCGCAATCAGCTTCGTAATTCGATGTCATCATAG 1320
QY 1321 ATGATGAATTCATCGAGCAATGCAATCAGTCAAAATATCCTCGCAAGGTATGTAATTT 1380
Db 1321 ATGATGAATTCATCGAGCAATGCAATCAGTCAAAATATCCTCGCAAGGTATGTAATTT 1380
QY 1381 GATTGAACAATCGCGACTTCTTTCAAC 1407
Db 1381 GATTGAACAATCGCGACTTCTTTCAAC 1407
```

RESULT 3

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US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
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; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
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Query Match 100.0%; Score 1407; DB 3; Length 4403765;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1407; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACCTGGCTTCGACAGATCAAAATAGGCGCATCGGTGAGCATAGTACAGGTCTGTCGCGCA 60
Db 1696149 ACCTGGCTTCGACAGATCAAAATAGGCGCATCGGTGAGCATAGTACAGGTCTGTCGCGCA 1696208
QY 61 TCTTTGATCATCGGAATAAGATGTGAGGCAATTTAAAGAGAGAGCCACGCGGACTCGCGG 120
Db 1696209 TCTTTGATCATCGGAATAAGATGTGAGGCAATTTAAAGAGAGAGCCACGCGGACTCGCGG 1696268
QY 121 CATTCAGCATGTGAGCGTTCGATGTGAGCGCACCATTCGCTGTCCAAAGATTCA 180
Db 1696269 CATTCAGCATGTGAGCGTTCGATGTGAGCGCACCATTCGCTGTCCAAAGATTCA 1696328
QY 181 GAGGACATTTGAATATTCACCTCGGACGCTATAGTCCGCTCCCGATCTATGCGGCGG 240
Db 1696329 GAGGACATTTGAATATTCACCTCGGACGCTATAGTCCGCTCCCGATCTATGCGGCGG 1696388
QY 241 CGCAGATGAAGTCTGCTTCGCGCCGACCTTCGAAACGTAGTGGCGCGCGCACCATTT 300
Db 1696389 CGCAGATGAAGTCTGCTTCGCGCCGACCTTCGAAACGTAGTGGCGCGCGCACCATTT 1696448
QY 301 CGGGGAGACGTGATGCGGCTGTAATCAGTTTGAAGCCACCGCATCTAGTAGTCCA 360
Db 1696449 CGGGGAGACGTGATGCGGCTGTAATCAGTTTGAAGCCACCGCATCTAGTAGTCCA 1696508
QY 361 GTAGAGCCCCATAGCCACAGCCTAGATCGTTGATCGAAATGGTTCGCGGCAATGACAA 420
Db 1696509 GTAGAGCCCCATAGCCACAGCCTAGATCGTTGATCGAAATGGTTCGCGGCAATGACAA 1696568
QY 421 TCGCACACAGCTGTTCAAAAGCCGACCTGCGCGCTTCGCGCTTCGCGTTCCAAATCGACCGCG 480
Db 1696569 TCGCACACAGCTGTTCAAAAGCCGACCTGCGCGCTTCGCGCTTCGCGTTCCAAATCGACCGCG 1696628
QY 481 GCGGTTGCGGTCGTTTCGATGCGGTTTCGATGCGGTTTCGATGCGGTTTCGATGCGGTTTCG 540
Db 1696629 GCGGTTGCGGTCGTTTCGATGCGGTTTCGATGCGGTTTCGATGCGGTTTCGATGCGGTTTCG 1696688
QY 541 CGTTGCGTCTTCGCGCATGAGCTGCTCAGATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 600
Db 1696689 CGTTGCGTCTTCGCGCATGAGCTGCTCAGATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1696748
QY 601 GTCCGAGACTATACCTTTCAACAGTTGTCATCCGAGGCTGCGCGGCAATGACCCAAAA 660
Db 1696749 GTCCGAGACTATACCTTTCAACAGTTGTCATCCGAGGCTGCGCGGCAATGACCCAAAA 1696808
QY 661 CCCGCGGCAAGGTTTCGCGGAGCAAGGAGCGTGGAGACGATAGATAATTTCACTGCGCA 720
Db 1696809 CCCGCGGCAAGGTTTCGCGGAGCAAGGAGCGTGGAGACGATAGATAATTTCACTGCGCA 1696868
QY 721 CAGTACCTCAAATAGTCCGAGGCTCGGCTCCGACGTTAAAGAGCAGATCCAGAATCGAC 780
Db 1696869 CAGTACCTCAAATAGTCCGAGGCTCGGCTCCGACGTTAAAGAGCAGATCCAGAATCGAC 1696928
QY 781 ACAGCGGCTCGAACCCTCCCAAAATGCTTAAATCGCGGTAGCGGTAGATTAATCGAAC 840
Db 1696929 ACAGCGGCTCGAACCCTCCCAAAATGCTTAAATCGCGGTAGCGGTAGATTAATCGAAC 1696988
QY 841 CAAAGTTACCGGATGCTAGTTCGTCGAAACACGCGCTCATCGACATACGAAACGGGTGAG 900
Db 1696989 CAAAGTTACCGGATGCTAGTTCGTCGAAACACGCGCTCATCGACATACGAAACGGGTGAG 1697048
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QY 901 RGGCCAGAGACATATTCGGTCCGTCGGCCCTGTTGGCAGAGGTTGGCCAGTCTCTCGGTC 960
Db 1697049 GGGCCAGAGACATATTCGGTCCGTCGGCCCTGTTGGCAGAGGTTGGCCAGTCTCTCGGTC 1697108
QY 961 TTGGCCGTGGCTAAATTCGTAGTCCACAGAAATTTGCCAGTCCGCTGCTGATACCGAGATAA 1020
Db 1697109 TTGGCCGTGGCTAAATTCGTAGTCCACAGAAATTTGCCAGTCCGCTGCTGATACCGAGATAA 1697168
QY 1021 CTGCAAAATCGCAATCAATAGACCCCTGTTGAGTAAAGAAAGATTCGTGTGCTTCTTCG 1080
Db 1697169 CTGCAAAATCGCAATCAATAGACCCCTGTTGAGTAAAGAAAGATTCGTGTGCTTCTTCG 1697228
QY 1081 AGGTAATCGGCGCGAGCCAGTCAGGATCTCGGCAAAATGAGCGCCGCGCTGAGTTG 1140
Db 1697229 AGGTAATCGGCGCGAGCCAGTCAGGATCTCGGCAAAATGAGCGCCGCGCTGAGTTG 1697288
QY 1141 AATTTCTAGTGGCCGCGAGTCGGCTTTCCGCCCAATCGTCCGTCGATCAGCGTCTCACGT 1200
Db 1697289 AATTTCTAGTGGCCGCGAGTCGGCTTTCCGCCCAATCGTCCGTCGATCAGCGTCTCACGT 1697348
QY 1201 ATCTTTTGATGAAACGTCCTTCACTGGACGGGAACAGTTATCCACTGTAAACCCCTGG 1260
Db 1697349 ATCTTTTGATGAAACGTCCTTCACTGGACGGGAACAGTTATCCACTGTAAACCCCTGG 1697408
QY 1261 CTCGTTTTGATCGAATTCCTTTGTCGCGCAATCAGCGTTGGTATATGCAATGATCATAG 1320
Db 1697409 CTCGTTTTGATCGAATTCCTTTGTCGCGCAATCAGCGTTGGTATATGCAATGATCATAG 1697468
QY 1321 ATGATGAATTCATCGACGAATCAATCAGTCAAAATATCCTCGCCAAAGGTATGTAATTT 1380
Db 1697469 ATGATGAATTCATCGACGAATCAATCAGTCAAAATATCCTCGCCAAAGGTATGTAATTT 1697528
QY 1381 GATTGAACAAATCGGACTTTCTTCTCAAC 1407
Db 1697529 GATTGAACAAATCGGACTTTCTTCTCAAC 1697555

RESULT 4
US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match 100.0%; Score 1407; DB 3; Length 4411529;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1407; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACCTGGCTTGACAGATCAAAATAGGGCCGATGGGTGACATAGTACAGGTCTGTCGCGCA 60
Db 1696015 ACCTGGCTTGACAGATCAAAATAGGGCCGATGGGTGACATAGTACAGGTCTGTCGCGCA 1696074
QY 61 TCTTTGATCGATCGGAATTAAGATGTGAGGCAATTTAAAGAGAAGCCACCGCGACTCGCGG 120
Db 1696075 TCTTTGATCGATCGGAATTAAGATGTGAGGCAATTTAAAGAGAAGCCACCGCGACTCGCGG 1696134
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QY 121 CATTGAGCATGTCGAGCGTCCGCTTCGATGCTGAGCGCAACATTCGCTGTCCAAAGATTCTCA 180
Db 1696135 CATTGAGCATGTCGAGCGTCCGCTTCGATGCTGAGCGCAACATTCGCTGTCCAAAGATTCTCA 1696194
QY 181 GACGAAACATTGAATATTCACATCGCGAGACGCTATAGTCCGCTCCCGATCTATGCGCGCG 240
Db 1696195 GACGAAACATTGAATATTCACATCGCGAGACGCTATAGTCCGCTCCCGATCTATGCGCGCG 1696254
QY 241 CGCAGATGAAGTCTCGGTTCCGCCGACCTTCGAAAGCTAGTGGCGCGCGCGCAACATTT 300
Db 1696255 CGCAGATGAAGTCTCGGTTCCGCCGACCTTCGAAAGCTAGTGGCGCGCGCGCAACATTT 1696314
QY 301 CGGGGAGACGTCGATCGCGGTGAATCAGTTTTGAAGCCACGCGCATCTAGTAGTCCA 360
Db 1696315 CGGGGAGACGTCGATCGCGGTGAATCAGTTTTGAAGCCACGCGCATCTAGTAGTCCA 1696374
QY 361 GTAGAGCCCCATAGCACAGCCTAGATCGTTGATCGAAATGGGTCGCGCGCATTTGACAA 420
Db 1696375 GTAGAGCCCCATAGCACAGCCTAGATCGTTGATCGAAATGGGTCGCGCGCATTTGACAA 1696434
QY 421 TCGGCAACAGCTGGTCAAGCGCAACGCTCGCCGCTTCGCGCTTCGATCGAATCGACGCCG 480
Db 1696435 TCGGCAACAGCTGGTCAAGCGCAACGCTCGCCGCTTCGCGCTTCGATCGAATCGACGCCG 1696494
QY 481 GCGGCTGCGGTGCTTCGAGTTTCGATCGCTAGTAAACGGGCCACGTCAGCGAGCATGTT 540
Db 1696495 GCGGCTGCGGTGCTTCGAGTTTCGATCGCTAGTAAACGGGCCACGTCAGCGAGCATGTT 1696554
QY 541 CTTTCGCTCTTCGCGCATGAAAGCTGCTCACCAGTTTGTGTGTGGGCTCGGTGCGTGG 600
Db 1696555 CTTTCGCTCTTCGCGCATGAAAGCTGCTCACCAGTTTGTGTGTGGGCTCGGTGCGTGG 1696614
QY 601 GTCCGAGACTATACCTTCAACAGTTGCAATGTCGAGGTCGCGCGGCAATGACCCAAAAA 660
Db 1696615 GTCCGAGACTATACCTTCAACAGTTGCAATGTCGAGGTCGCGCGGCAATGACCCAAAAA 1696674
QY 661 CCGCGCGGACGTTTCGCGAGCAAGGAGCGTGGAGAGATAGATAATTTTCACTGGCGCA 720
Db 1696675 CCGCGCGGACGTTTCGCGAGCAAGGAGCGTGGAGAGATAGATAATTTTCACTGGCGCA 1696734
QY 721 CAGTACCTCAAAATAGTCCGAGCCTCGGCTCCGAGCTTAAAGAGCAGATCCAGAAATCGAC 780
Db 1696735 CAGTACCTCAAAATAGTCCGAGCCTCGGCTCCGAGCTTAAAGAGCAGATCCAGAAATCGAC 1696794
QY 781 ACGCGGGCTCGAAACCTCCCAATTCCTTATTAATTCGCGGTAGCCGTATATCGCAAC 840
Db 1696795 ACGCGGGCTCGAAACCTCCCAATTCCTTATTAATTCGCGGTAGCCGTATATCGCAAC 1696854
QY 841 CAAAGTTACCCGATGCTAAGTTTCGTCGAACACGCGCTCATCGACATACGAAACGGGCTGAG 900
Db 1696855 CAAAGTTACCCGATGCTAAGTTTCGTCGAACACGCGCTCATCGACATACGAAACGGGCTGAG 1696914
QY 901 GGGCCAGAGACATATTCGGTCCGCTCGGCTGTTGGCAGAGGTTGGCCAGTCTCTCGGTC 960
Db 1696915 GGGCCAGAGACATATTCGGTCCGCTCGGCTGTTGGCAGAGGTTGGCCAGTCTCTCGGTC 1696974
QY 961 TTGCGGTGGCTAAATTCGTAGTCCCAAGAAATTTGCCAGTCCGCTGATACCGAGATAA 1020
Db 1696975 TTGCGGTGGCTAAATTCGTAGTCCCAAGAAATTTGCCAGTCCGCTGATACCGAGATAA 1697034
QY 1021 CTGCAAAATCGCAATCAATAGACGCTGTTGAGTAAAGAAAGATTCGTGTGCTTCTTCG 1080
Db 1697035 CTGCAAAATCGCAATCAATAGACGCTGTTGAGTAAAGAAAGATTCGTGTGCTTCTTCG 1697094
QY 1081 AGGTAATCGGCGCGAGCCAGTCAGCGATCTCCGCAAAATGAGCGCCGCGCTGATTTG 1140
Db 1697095 AGGTAATCGGCGCGAGCCAGTCAGCGATCTCCGCAAAATGAGCGCCGCGCTGATTTG 1697154
QY 1141 AATTTCTAGTGGCCGCGAGTCGCTTTGCGCCAAATCGGTGCGCTGATACGCGTCTCACGT 1200
Db 1697155 AATTTCTAGTGGCCGCGAGTCGCTTTGCGCCAAATCGGTGCGCTGATACGCGTCTCACGT 1697214
QY 1201 ATCTTTTGATGAAACGTCCTTCACTGGACGGGAACAGTTATCCACTGTAAACCCCTGG 1260
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Db 1697215 ATCTTTTGTGAAACGTCCTTCCCTGACGCGAACAAGTTATCCACTGTAAACCCCTGG 1697274
QY 1261 CTCGTTTTTCATCGAATTCCTGTTTCCCAATCACGCTTCGTTATATGCGATGCATCATAG 1320
Db 1697275 CTCGTTTTTCATCGAATTCCTGTTTCCCAATCACGCTTCGTTATATGCGATGCATCATAG 1697334
QY 1321 ATGATGAATTCATCGACGAATCAATCAGGTCAAAATATCCTCGCCAAAGGTATGTAATTT 1380
Db 1697335 ATGATGAATTCATCGACGAATCAATCAGGTCAAAATATCCTCGCCAAAGGTATGTAATTT 1697394
QY 1381 GATTGAACCAATCGCGACTTTCTTCAAC 1407
Db 1697395 GATTGAACCAATCGCGACTTTCTTCAAC 1697421

RESULT 5

US-09-894-844-44/c
; Sequence 44, Application US/09894844
; Patent No. 6686166
; GENERAL INFORMATION:
; APPLICANT: Behr, Marcel
; APPLICANT: Small, Peter
; APPLICANT: Schoolnik, Gary
; APPLICANT: Wilson, Michael A.
; TITLE OF INVENTION: Molecular Differences Between Species of
; TITLE OF INVENTION: the M. Tuberculosis Complex
; FILE REFERENCE: STAN102CON
; CURRENT APPLICATION NUMBER: US/09/894,844
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/318,191
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 60/097,936
; PRIOR FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 693
; TYPE: DNA
; ORGANISM: Mycobacteria tuberculosis
US-09-894-844-44

Query Match 49.3%; Score 693; DB 3; Length 693;
Best Local Similarity 100.0%; Pred. No. 4.9e-216;
Matches 693; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 714 CTGGGACAGTACCTCAATAGTTCGGAGCCTCGGCTCCGAGCTTAAAGACAGATCCAG 773
Db 693 CTGGGACAGTACCTCAATAGTTCGGAGCCTCGGCTCCGAGCTTAAAGACAGATCCAG 634
QY 774 AATCGACAGCGGGCTCGAACCCTCCCAATTCCTTATATCGGGTAGCCGTCATA 833
Db 633 AATCGACAGCGGGCTCGAACCCTCCCAATTCCTTATATCGGGTAGCCGTCATA 574
QY 834 ATCGAACCAAGTTACCCGGATGTAAGTTTCGTGCAACAGCGCTCATCGACATACGAACG 893
Db 573 ATCGAACCAAGTTACCCGGATGTAAGTTTCGTGCAACAGCGCTCATCGACATACGAACG 514
QY 894 GCGTAGGGGCGCAGACATATTCGTCGCTCGCGCTGTGGCAGAGTTGGCCAGTCT 953
Db 513 GCGTAGGGGCGCAGACATATTCGTCGCTCGCGCTGTGGCAGAGTTGGCCAGTCT 454
QY 954 CTCGGTCTTCGGCTCGGCTAATTCGTAGTCCCAAGAAATTCGACGTCGGTCTGTATACC 1013
Db 453 CTCGGTCTTCGGCTCGGCTAATTCGTAGTCCCAAGAAATTCGACGTCGGTCTGTATACC 394
QY 1014 GAGATAACTGCAATCGCAATCAATAGACGCTGTTGAGTAAGGAAGATTCGTGTGCTG 1073
Db 393 GAGATAACTGCAATCGCAATCAATAGACGCTGTTGAGTAAGGAAGATTCGTGTGCTG 334
QY 1074 TTCTTCGAGGTAATCGGCGCGAGCGAGTCAGCATCTCCGCAAAATGAGCGCGCGCGCT 1133
Db 333 TTCTTCGAGGTAATCGGCGCGAGCGAGTCAGCATCTCCGCAAAATGAGCGCGCGCGCT 274

QY 1134 GTAGTTGAATTCAGTCCCGCCAGTGGCTTTTCGCCAATCGGTGCCGTCGATCAGCGT 1193
Db 273 GTAGTTGAATTCAGTCCCGCCAGTGGCTTTTCGCCAATCGGTGCCGTCGATCAGCGT 214
QY 1194 CTCAGGTATCTTTTGAATGAGAAACGTCCTTCACCTGAGAGCGGAAACAGTTATCCACTGTAA 1253
Db 213 CTCAGGTATCTTTTGAATGAGAAACGTCCTTCACCTGAGAGCGGAAACAGTTATCCACTGTAA 154
QY 1254 CCCCTGGCTCGTTTGAATCCGATTTCTGTTTCGCAATCACGCTTGGTATATTCATGCTC 1313
Db 153 CCCCTGGCTCGTTTGAATCCGATTTCTGTTTCGCAATCACGCTTGGTATATTCATGCTC 94
QY 1314 ATCATAGATGATGAATTCATCGACGAATCAATCAGGTCAAAATATCTCCGCAAGGTAT 1373
Db 93 ATCATAGATGATGAATTCATCGACGAATCAATCAGGTCAAAATATCTCCGCAAGGTAT 34
QY 1374 GTAATTTGATGAACAAATCGGACTTTCTTCAA 1406
Db 33 GTAATTTGATGAACAAATCGGACTTTCTTCAA 1

RESULT 6

US-09-894-844-43/c
; Sequence 43, Application US/09894844
; Patent No. 6686166
; GENERAL INFORMATION:
; APPLICANT: Behr, Marcel
; APPLICANT: Small, Peter
; APPLICANT: Schoolnik, Gary
; APPLICANT: Wilson, Michael A.
; TITLE OF INVENTION: Molecular Differences Between Species of
; TITLE OF INVENTION: the M. Tuberculosis Complex
; FILE REFERENCE: STAN102CON
; CURRENT APPLICATION NUMBER: US/09/894,844
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/318,191
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 60/097,936
; PRIOR FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 498
; TYPE: DNA
; ORGANISM: Mycobacteria tuberculosis
US-09-894-844-43

Query Match 30.3%; Score 427; DB 3; Length 498;
Best Local Similarity 100.0%; Pred. No. 4.5e-129;
Matches 427; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACCTCGCTTCGACAGATCAATAGGCGCATGGGTACGATAGTACAGGTCTCGCGCA 60
Db 427 ACCTCGCTTCGACAGATCAATAGGCGCATGGGTACGATAGTACAGGTCTCGCGCA 368
QY 61 TCTTTGATGATCGGATTAAGATGTCAGGCAATTAAGAGAGCCACCGCGACTCGCGG 120
Db 367 TCTTTGATGATCGGATTAAGATGTCAGGCAATTAAGAGAGCCACCGCGACTCGCGG 308
QY 121 CATTGAGATGTCGAGCGTCGCTTCGATGTGAGCGCACCATTTCCGTTGTCACAGATTCA 180
Db 307 CATTGAGATGTCGAGCGTCGCTTCGATGTGAGCGCACCATTTCCGTTGTCACAGATTCA 248
QY 181 GACGAACATGTAATATTCACATCGCGAOGCTATAGTCGCGCTCCCGATCTATGCGCGCG 240
Db 247 GACGAACATGTAATATTCACATCGCGAOGCTATAGTCGCGCTCCCGATCTATGCGCGCG 188
QY 241 CGCAGATGAGTCTCGGTCGCGCGGACCTTCGAAAGTAGTCGCGCGCGCGCACCATTT 300
Db 187 CGCAGATGAGTCTCGGTCGCGCGGACCTTCGAAAGTAGTCGCGCGCGCGCACCATTT 128
QY 301 CGGGGAGACGTCGATCGCGGTGTAATCAGTTTGAAGCCACGCGCATCTAGGTAGTCCA 360

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Db 127 CGGGGAGACGTCGATCCGGTGTAATCAGTTTGAAGCCACGCGCATCTAGTAGTCCA 68
QY 361 GTAGAGCCCATAGCCACAGCCTAGATCGTTGATCGAAAATGGTCCGCCGATTGACAA 420
Db 67 GTAGAGCCCATAGCCACAGCCTAGATCGTTGATCGAAAATGGTCCGCCGATTGACAA 8
QY 421 TCGGCAC 427
Db 7 TCGGCAC 1

RESULT 7
US-09-543-681A-4167/c
; Sequence 4167, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 4167
; LENGTH: 702
; TYPE: DNA
; ORGANISM: Proteus mirabilis
US-09-543-681A-4167

Query Match 3.6%; Score 50.4; DB 3; Length 702;
Best Local Similarity 55.8%; Pred. No. 9.2e-06;
Matches 96; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

QY 1234 GGAACAGTTATCCACTGTAAACCCTGGCTCGTTTTCGATCGGATTTCTGTTTCGCCAATCA 1293
Db 173 GGAATAGTAATAATTTGTGGACCAATTCCTAGTTTGAATTCGATTTCTATTATATATATCA 114
QY 1294 CGCTTGGTATATGCAATGTCATCATAGATGATGAATTCATCGACGAATGCAATCAGGTCA 1353
Db 113 CTTTAAATATAATTACATCATCAATAAATAATAATATATATCGTATGATAAGCTAATGCA 54
QY 1354 AAATATCTCCGCCAAGGTATGTAATTTGATGAACAATCGGACTTTCTTCA 1405
Db 53 TAATATCCTATATATGGAATAAGTAAGTTGCAATACAGCTAATATATATAA 2

RESULT 8
US-09-949-016-13678
; Sequence 13678, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13678
; LENGTH: 18037
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13678
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Query Match 2.8%; Score 39.8; DB 3; Length 18037;
Best Local Similarity 48.1%; Pred. No. 0.117;
Matches 113; Conservative 0; Mismatches 122; Indels 0; Gaps 0;

QY 411 GCATTGACAATCGGCACACAGCTGGTCAAGCGCAACCCCTGCGCGCTTCGGCGTTCCAA 470
Db 3848 GCCTAGGGCTCGGCAGCTGTGACCAAGCGGGGCCACCTGCGCTCTGAGCCCTGCCAG 3907
QY 471 TCGACCGCGCGCGGGTGGCTGTGCTTCGAGTTTTCGATCGTAGTAACGGGCCACGTCAG 530
Db 3908 GTGCAGCCGAGCCAGAGCCCTGGCGTGGAGGTGAGTGGCAGCCAGAGGGCTGGTGAG 3967
QY 531 CGAGCATGCTGTTGGCTTTCGGCCATGAAGCTGCTACCATTTGTTGTGTGTGGCGCT 590
Db 3968 AGTGGCTGTTTCTCCCAACAGCTGACTTTTGGGGTGTCAAGCGAGCTGACAGCGTCTGTGG 4027
QY 591 CGGTGCGTGGTCCGAGACTATACCTTCAACAGTTTGCATGCCGAGGCTCGCGCG 645
Db 4028 CCAAGAGGAGTCTTTCATTGGGACTTCCCTACTGTTGAGGCTGCGCTGGGCGG 4082

RESULT 9
US-09-902-540-6354/c
; Sequence 6354, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 6354
; LENGTH: 702
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-6354

Query Match 2.5%; Score 35.8; DB 3; Length 702;
Best Local Similarity 56.3%; Pred. No. 0.55;
Matches 67; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 203 CGGAGCGCTATAGTCGGCTCCCGATCTATGCGCGCGCAGATGAAGTCTCGGTTCCG 262
Db 225 CGCGTGAACGACTCCGGCTCCGGAAGGATGCGCGGCTCGCACGAAGACGGGTCTC 166
QY 263 CGGACCTTCGAAACGTAGTGGCGCGCGCCACCATTTTCGGGGGAGACCTTCGATGCGG 321
Db 165 CAGCGCTCTCTCAGACACACCCGCGCGGCTCTCTCTTGGAGAAGCGGATGG 107

RESULT 10
US-09-902-540-408/c
; Sequence 408, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
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/ SEQ ID NO 408
/ LENGTH: 1583
/ TYPE: DNA
/ ORGANISM: Myxococcus xanthus
US-09-902-540-408

Query Match      2.5%; Score 35.8; DB 3; Length 1583;
Best Local Similarity 56.3%; Pred. No. 0.87;
Matches 67; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 203 CGGAGCGTATAGTCCGCTCCCGATCTATGCGCGCGGCAGATGAAGTCTGCGTTCCG 262
Db 1106 CGGCTGAACGACTCCGCTCCGGAAGGATGCGCGGCTCGCACGAAGACGGGTCTC 1047

QY 263 CGGACCTTCGAAACGTAAGTGGCGCGCGCCGACCATTTTCGGGGGAGACGTCGATGCCG 321
Db 1046 CAGCCGCTCTCAGACACACCGCGCGCGGGGCTCTCTTGGAGAAAGCGGATGG 988

RESULT 11
US-09-949-016-16832/c
/ Sequence 16832, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ CURRENT FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 16832
/ LENGTH: 5992
/ TYPE: DNA
/ ORGANISM: Human
US-09-949-016-16832

Query Match      2.5%; Score 35.8; DB 3; Length 5992;
Best Local Similarity 51.1%; Pred. No. 1.8; Indels 6; Gaps 1;
Matches 113; Conservative 0; Mismatches 102; Indels 6; Gaps 1;

QY 75 GAATAAGATGTTCAGGCAATTAAAGAGAGAGCCAGCGGACTCGCGGCATTCAGCATGTGC 134
Db 3344 GAGGAAGCTGGGTACACACAGCCAGAGAGCGGGGAAACGGGGCATCTAACTAGGAC 3285.

QY 135 AGCGTCGCTTCA-----TGTGAGCGCACCAATTCGTCGTCACAAAGATTTCAGACGAACA 188
Db 3284 ACAGTCGCATCAGGGGTGAGTACCTGACCTTACAGGCGCCACCACTTCAGACTGAGA 3225

QY 189 TTGAATATTCCTCGCGAGCTATAGTCCGCTCCCGATCTATGCGCGCGCGCAGATG 248
Db 3224 TGGAAACGCGCTCTGGGAGAACCTGATCCGCCCCACCTACACAGGCCCCGAGGTACT 3165

QY 249 AAGTCTGCGCTTCGCGGACCTTCGAAACGTAAGTGGCGCGC 289
Db 3164 GGGCTGCGCGCCACACCTTGGCGCGAGTGGGCTCTGC 3124

RESULT 12
US-09-949-016-16833
/ Sequence 16833, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ CURRENT FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 16832
/ LENGTH: 5992
/ TYPE: DNA
/ ORGANISM: Human
US-09-949-016-16832

Query Match      2.5%; Score 35.8; DB 3; Length 5992;
Best Local Similarity 51.1%; Pred. No. 1.8; Indels 6; Gaps 1;
Matches 113; Conservative 0; Mismatches 102; Indels 6; Gaps 1;

QY 75 GAATAAGATGTTCAGGCAATTAAAGAGAGAGCCAGCGGACTCGCGGCATTCAGCATGTGC 134
Db 3344 GAGGAAGCTGGGTACACACAGCCAGAGAGCGGGGAAACGGGGCATCTAACTAGGAC 3285.

QY 135 AGCGTCGCTTCA-----TGTGAGCGCACCAATTCGTCGTCACAAAGATTTCAGACGAACA 188
Db 3284 ACAGTCGCATCAGGGGTGAGTACCTGACCTTACAGGCGCCACCACTTCAGACTGAGA 3225

QY 189 TTGAATATTCCTCGCGAGCTATAGTCCGCTCCCGATCTATGCGCGCGCGCAGATG 248
Db 3224 TGGAAACGCGCTCTGGGAGAACCTGATCCGCCCCACCTACACAGGCCCCGAGGTACT 3165

QY 249 AAGTCTGCGCTTCGCGGACCTTCGAAACGTAAGTGGCGCGC 289
Db 3164 GGGCTGCGCGCCACACCTTGGCGCGAGTGGGCTCTGC 3124

RESULT 13
US-09-902-540-3161/c
/ Sequence 3161, Application US/09902540
/ Patent No. 6833447
/ GENERAL INFORMATION:
/ APPLICANT: Goldman, Barry S.
/ APPLICANT: Hinkle, Gregory J.
/ APPLICANT: Slater, Steven C.
/ APPLICANT: Wiegand, Roger C.
/ TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
/ FILE REFERENCE: 38-10(15849)B
/ CURRENT APPLICATION NUMBER: US/09/902,540
/ CURRENT FILING DATE: 2001-07-10
/ PRIOR APPLICATION NUMBER: 60/217,883
/ PRIOR FILING DATE: 2000-07-10
/ NUMBER OF SEQ ID NOS: 16825
/ SEQ ID NO 3161
/ LENGTH: 978
/ TYPE: DNA
/ ORGANISM: Myxococcus xanthus
US-09-902-540-3161

Query Match      2.5%; Score 35.6; DB 3; Length 978;
Best Local Similarity 57.0%; Pred. No. 0.77;
Matches 65; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 215 GTCCGCTCCCGATCTATGCGCGCGGCAGATGAAGTCTGCGTTCGCCGACCTTCGAA 274
Db 531 GTCCGCTTCGCTCGCTCGCTCACCAGCGCATGACGCGTTCGCGCGCGGCCAC 472

QY 275 ACGTAGTGGCGCGCGGCACCACTTCGGGGGAGAGCTCGATCCCGGTGAATC 328
Db 471 CTGCACCGCGCGCGTGGCCACGCTCCCGCGCGCATGGACACGACGCTCTC 418
```

RESULT 14

US-09-902-540-1144
; Sequence 1144, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1144
; LENGTH: 16350
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; US-09-902-540-1144

Query Match 2.5%; Score 35.6; DB 3; Length 16350;
Best Local Similarity 57.0%; Pred. No. 3.8;
Matches 65; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 215 GTCGCGCTCCGATCTATCGCGCGCGCAGATGAAGTCTGGGTTGCGCCGACCTTCGAA 274
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Db 3602 GTCGCGCTTGGCTGCTGCTCACCACGCGGATGAGCGTGCTTCGCGCGCGGCCAC 3661
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QY 275 ACGTAGTGGCGCGCGCGCACCATTTCCGGGGAGAGCTGATGCGCGTGAATC 328
|||||
Db 3662 CTGCACCGCGCGGTGCCACGCTCCCGCGGCGCATGGACACGACGCTCTC 3715
|||||

RESULT 15

US-09-949-016-177875
; Sequence 177875, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 177875
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-177875

Query Match 2.5%; Score 35.4; DB 3; Length 601;
Best Local Similarity 50.7%; Pred. No. 0.68;
Matches 112; Conservative 1; Mismatches 102; Indels 6; Gaps 1;

QY 75 GAATAAGATGTACGGCAATTAAGAAGAGACCCACGCGGACTCGCGCATTCAGCATGTCG 134
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Db 218 GAGGAAGCTGGGTCAACACAGCCCAAGAGAGGGGGAAACGGGGCATCTAAGTAGGAC 277
|||||

QY 135 AGCGTCGCTTCGA-----TGTGAGCGCACCAATTCGTTCCAAACGATTTACAGACGAACA 188
|||||
Db 278 ACAGTCGCATCCAGGGGTGAGTCRCCTGACCTACAGGGGCCACACCACTTCAGACTGAGA 337
|||||

QY 189 TTGAATATTCACCTCGCAGCGGTATAGTCCGCTCCCGATCTATGCGCGCGCGCAGATG 248
|||||

Db 338 TGGAAACGCCCTCTTGGGAGAACCTGTATCCGCCCCACCCCTACACAGGCCCGAGGTACT 397
|||||
QY 249 AAGTCTGGGTTTCGCCCGGACCTTTCGAAACGTAGTGGGGCGC 289
|||||
Db 398 GGGCTTGGCGCGCCACACCTTGGCGCGGAGTGGGCTCTGC 438
|||||

Search completed: February 19, 2006, 20:42:05
Job time : 274.821 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 20, 2006, 01:31:10 ; Search time 1208.87 Seconds
(without alignments)
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Perfect score: 1407

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA Main:*

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- 2: /cgn2_6/prodata/1/pubpna/US08_PUBCOMB.seq.*
- 3: /cgn2_6/prodata/1/pubpna/US09A_PUBCOMB.seq.*
- 4: /cgn2_6/prodata/1/pubpna/US09B_PUBCOMB.seq.*
- 5: /cgn2_6/prodata/1/pubpna/US10A_PUBCOMB.seq.*
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- 8: /cgn2_6/prodata/1/pubpna/US10D_PUBCOMB.seq.*
- 9: /cgn2_6/prodata/1/pubpna/US10E_PUBCOMB.seq.*
- 10: /cgn2_6/prodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1407	100.0	12732	6	US-10-259-678-1
2	693	49.3	693	3	US-09-894-844-44
3	693	49.3	693	7	US-10-388-902-44
4	693	49.3	693	7	US-10-647-089-44
5	427	30.3	498	3	US-09-894-844-43
6	427	30.3	498	7	US-10-388-902-43
7	427	30.3	498	7	US-10-647-089-43
8	39.8	2.8	27204	5	US-10-087-192-1528
9	38.4	2.7	2464	9	US-10-521-103-1
10	37.8	2.7	536	7	US-10-338-110-119
11	37.8	2.7	894	6	US-10-156-761-1933
12	37.8	2.7	9025608	6	US-10-156-761-1
13	36.6	2.6	485	7	US-10-437-963-48583
14	36.2	2.6	783	6	US-10-156-761-2972
15	36	2.6	1126	7	US-10-425-114-34546
16	36	2.6	1188	8	US-10-425-115-62490
17	35.8	2.5	17138	8	US-10-741-600-18009
18	35.6	2.5	1662	7	US-10-437-963-12650
19	35.4	2.5	622	4	US-09-925-065A-597843
20	35.4	2.5	727	9	US-10-956-157-3059
21	35.4	2.5	727	9	US-10-956-157-8294
22	35.4	2.5	1632	6	US-10-369-493-38385
23	35.4	2.5	4698	6	US-10-156-761-6923

C	24	35.4	2.5	9025608	6	US-10-156-761-1	Sequence 1, Appli
C	25	35.2	2.5	3683	6	US-10-369-493-35076	Sequence 35076, A
C	26	35	2.5	459	8	US-10-627-592-16	Sequence 16, Appl
C	27	35	2.5	1215	6	US-10-321-188-72	Sequence 72, Appl
C	28	35	2.5	1215	6	US-10-321-188-74	Sequence 74, Appl
C	29	35	2.5	1215	9	US-10-915-172-72	Sequence 72, Appl
C	30	35	2.5	1215	9	US-10-915-172-74	Sequence 74, Appl
C	31	35	2.5	1266	6	US-10-369-493-39313	Sequence 39313, A
C	32	35	2.5	1269	6	US-10-369-493-39688	Sequence 39688, A
C	33	35	2.5	1269	6	US-10-369-493-40041	Sequence 40041, A
C	34	35	2.5	1545	9	US-10-200-545-48	Sequence 48, Appl
C	35	34.8	2.5	1540	8	US-10-425-115-167794	Sequence 167794, A
C	36	34.8	2.5	1554	7	US-10-282-122A-14480	Sequence 14480, A
C	37	34.6	2.5	388	4	US-09-925-065A-585977	Sequence 585977, A
C	38	34.6	2.5	496	4	US-09-925-065A-827710	Sequence 827710, A
C	39	34.6	2.5	671	5	US-10-184-644-346	Sequence 346, App
C	40	34.6	2.5	671	5	US-10-184-634-346	Sequence 346, App
C	41	34.6	2.5	810	7	US-10-767-701-9705	Sequence 9705, Ap
C	42	34.6	2.5	939	7	US-10-282-122A-13932	Sequence 13932, A
C	43	34.4	2.4	328	8	US-10-674-124A-5740	Sequence 5740, Ap
C	44	34.4	2.4	963	6	US-10-369-493-38385	Sequence 38385, A
C	45	34.4	2.4	963	6	US-10-369-493-38868	Sequence 38868, A

ALIGNMENTS

RESULT 1

US-10-259-678-1

; Sequence 1, Application US/10259678

; Publication No. US20030198974A1

; GENERAL INFORMATION:

; APPLICANT: Cole, Stewart

; APPLICANT: Buchrieser-Brosch, Roland

; APPLICANT: Gordon, Stephen

; APPLICANT: Billault, Alain

; TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM

; TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA

; TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA

; FILE REFERENCE: 3495-0169

; CURRENT APPLICATION NUMBER: US/10/259,678

; CURRENT FILING DATE: 2002-09-30

; PRIOR APPLICATION NUMBER: US/09/060,756

; PRIOR FILING DATE: 1998-04-16

; NUMBER OF SEQ ID NOS: 743

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 1

; LENGTH: 12732

; TYPE: DNA

; ORGANISM: Mycobacterium tuberculosis

US-10-259-678-1

Query Match 100.0%; Score 1407; DB 6; Length 12732;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1407; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ACCTCGCTTGAGAGATCAAAATAGCGGCATAGGTCGATAGTACAGTACAGTTCGTCGCGCA	60
Db	1	ACCTCGCTTGAGAGATCAAAATAGCGGCATAGGTCGATAGTACAGTTCGTCGCGCA	60
Qy	61	TCCTTTGATGATCGCAATAAGATGTCAGCAATTAAGAGAGAACGACGCGGACCTCGCGG	120
Db	61	TCCTTTGATGATCGCAATAAGATGTCAGCAATTAAGAGAGAACGACGCGGACCTCGCGG	120
Qy	121	CATTGAGATGTCGAGCGTCGCTTCGATGTAGCGCACCATTCGCTGTCCACGATTTCA	180
Db	121	CATTGAGATGTCGAGCGTCGCTTCGATGTAGCGCACCATTCGCTGTCCACGATTTCA	180
Qy	181	GACGAACATTAATTAATTCATCTCGGAGAGCTATAGTCGCGCTCCGATCTATGTCGCGCGG	240
Db	181	GACGAACATTAATTAATTCATCTCGGAGAGCTATAGTCGCGCTCCGATCTATGTCGCGCGG	240
Qy	241	CGCAGATGATGTCGCTCGGTCGCCACCTTCGAAACGATAGTCGCGCGCGCGCACCATTT	300

Db 241 |||||CGCAGATGAAGTCTGGGTTCCGCCGACCTTCGAAAGCTAGTGGCGCGCGCCACCAATTT 300
QY 301 CGGGGAGACGTCGATCGCGGTGTAATCAGTTTTGAAGCCACCGCGCATCTAGGTAGTCCA 360
Db 301 CGGGGAGACGTCGATCGCGGTGTAATCAGTTTTGAAGCCACCGCGCATCTAGGTAGTCCA 360
QY 361 GTAGAGCCCCATAGCCACAGCCTAGATCGTTGATCGAAAATGGTCCGCGCATTTGACAA 420
Db 361 GTAGAGCCCCATAGCCACAGCCTAGATCGTTGATCGAAAATGGTCCGCGCATTTGACAA 420
QY 421 TCGCACACAGCTGCTCAAAAGCGCAACCGCTCGCCGCTTTCGCGCTTCCCAATCGAGCGCGC 480
Db 421 TCGCACACAGCTGCTCAAAAGCGCAACCGCTCGCCGCTTTCGCGCTTCCCAATCGAGCGCGC 480
QY 481 CGGGGTGCGGTGCTTCGAGTTTTCGATGCTAGTAACGGGCGCACGTCAGCGAGCATGGT 540
Db 481 CGGGGTGCGGTGCTTCGAGTTTTCGATGCTAGTAACGGGCGCACGTCAGCGAGCATGGT 540
QY 541 CGTTGGTCTTCGCGCATGAAGTGCTCAGATTTGTGTGTGGCGCTCGGTGCGGTGG 600
Db 541 CGTTGGTCTTCGCGCATGAAGTGCTCAGATTTGTGTGTGGCGCTCGGTGCGGTGG 600
QY 601 GTCCGAGACTATACCTTCAACAGTTGCATGCCGAGCTGCGGGGCAATGACCCAAAAA 660
Db 601 GTCCGAGACTATACCTTCAACAGTTGCATGCCGAGCTGCGGGGCAATGACCCAAAAA 660
QY 661 CCGCGCGGCGACGGTTGCGCGAGCAAGAGCGTGGAGACGATAGATAAATTTCACTGGCGA 720
Db 661 CCGCGCGGCGACGGTTGCGCGAGCAAGAGCGTGGAGACGATAGATAAATTTCACTGGCGA 720
QY 721 CAGTACTCAAAATAGTCCGAGGCTCGGCTCCGACGTTTAAAGAGCAGATCCAGATCCGAC 780
Db 721 CAGTACTCAAAATAGTCCGAGGCTCGGCTCCGACGTTTAAAGAGCAGATCCAGATCCGAC 780
QY 781 ACGGGGGCTCAACCCCTCCACAAATTCGTTATATCGCGGTAGCCGTCATAATCGCAC 840
Db 781 ACGGGGGCTCAACCCCTCCACAAATTCGTTATATCGCGGTAGCCGTCATAATCGCAC 840
QY 841 CAAAGTTACCCGGATGCTAAGTTTCGTGAAACACGCGCTCATCGACATACGAAACGGGCTGAG 900
Db 841 CAAAGTTACCCGGATGCTAAGTTTCGTGAAACACGCGCTCATCGACATACGAAACGGGCTGAG 900
QY 901 GGGCCAGACATATTCGTCGCTCGGCTGTTGGCAGAGGTTGGCAGTCTCTCGGTC 960
Db 901 GGGCCAGACATATTCGTCGCTCGGCTGTTGGCAGAGGTTGGCAGTCTCTCGGTC 960
QY 961 TTGCGGTCGGCTAAATTCGTAGTCCACGAAATTTGCCAGTCCGCTGCTGATACCGAGATAA 1020
Db 961 TTGCGGTCGGCTAAATTCGTAGTCCACGAAATTTGCCAGTCCGCTGCTGATACCGAGATAA 1020
QY 1021 CTGCAAAATCGCAATCAATAGACGCTGTTGAGTAAGGAAAGATTGCTGTGCTGTTCTTCG 1080
Db 1021 CTGCAAAATCGCAATCAATAGACGCTGTTGAGTAAGGAAAGATTGCTGTGCTGTTCTTCG 1080
QY 1081 AGGTAAATCGGCGCAGCAGTACGATCTCCGCAAAATGACGCGCCGCGCTGTAGTTG 1140
Db 1081 AGGTAAATCGGCGCAGCAGTACGATCTCCGCAAAATGACGCGCCGCGCTGTAGTTG 1140
QY 1141 AATTTCTAGTCCGCGCAGTCCGCTTTCGCCCAATCGGTGCGCTCGATCAGCGTCTCAAGT 1200
Db 1141 AATTTCTAGTCCGCGCAGTCCGCTTTCGCCCAATCGGTGCGCTCGATCAGCGTCTCAAGT 1200
QY 1201 ATCTTTTGATGAAACGTCCTTCACTCGAGCGGAAACAGTTATCCACTGTAAACCCCTGG 1260
Db 1201 ATCTTTTGATGAAACGTCCTTCACTCGAGCGGAAACAGTTATCCACTGTAAACCCCTGG 1260
QY 1261 CTCGTTTGTATCCGATTTCTGTTTCGCCCAATCACGCTTGGTATATTCGATGTCATCATAG 1320
Db 1261 CTCGTTTGTATCCGATTTCTGTTTCGCCCAATCACGCTTGGTATATTCGATGTCATCATAG 1320
QY 1321 ATGATCAATTCATCGACGAATCGAATCAGGTCAAAATATCCTCGCCAGGATGTAATTT 1380

Db 1321 ATGATCAATTCATCGACGAATCAATCAGGTCAAAATATCCTCGCCAGGTATGTAATTT 1380
QY 1381 GATTGAACAATCGGACTTTTCTTCAAC 1407
Db 1381 GATTGAACAATCGGACTTTTCTTCAAC 1407
RESULT 2
US-09-894-844-44/c
; Sequence 44, Application US/098994844
; Patent No. US20020176873A1
; GENERAL INFORMATION:
; APPLICANT: Behr, Marcel
; APPLICANT: Small, Peter
; APPLICANT: Schoolnik, Gary
; APPLICANT: Wilson, Michael A.
; TITLE OF INVENTION: Molecular Differences Between Species of
; FILE REFERENCE: STAN102CON
; CURRENT APPLICATION NUMBER: US/09/894,844
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/318,191
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 60/097,936
; PRIOR FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 693
; TYPE: DNA
; ORGANISM: Mycobacteria tuberculosis
US-09-894-844-44
Query Match 49.3%; Score 693; DB 3; Length 693;
Best Local Similarity 100.0%; Pred. No. 3.7e-227;
Matches 693; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 714 CTGGGCGACGATGACCTCAAAATAGTCCGAGCCTCGGCTCCGAGCGATTTAAAGAGCAGATCCAG 773
Db 693 CTGGGCGACGATGACCTCAAAATAGTCCGAGCCTCGGCTCCGAGCGATTTAAAGAGCAGATCCAG 634
QY 774 AATCGACACGGCGGCTCGAACCCCTCCACAAATTCGTTATATCGCGGTAGCCGTCATA 833
Db 633 AATCGACACGGCGGCTCGAACCCCTCCACAAATTCGTTATATCGCGGTAGCCGTCATA 574
QY 834 ATCGAAACCAAGTTACCCGGATGCTAAGTTTCGTGAAACACGCGCTCATCGACATACGAAACG 893
Db 573 ATCGAAACCAAGTTACCCGGATGCTAAGTTTCGTGAAACACGCGCTCATCGACATACGAAACG 514
QY 894 GGCTGAGGGGCGACAGACATATTCGGTCTCGTGGCGCTGTTGGCAGAGGTTGGCCAGTCT 953
Db 513 GGCTGAGGGGCGACAGACATATTCGGTCTCGTGGCGCTGTTGGCAGAGGTTGGCCAGTCT 454
QY 954 CTCGGTCTTCGGCTCGGCTAATTCGTCAGTCCACGAAATTCGCGTCCGCTGCTGATACC 1013
Db 453 CTCGGTCTTCGGCTCGGCTAATTCGTCAGTCCACGAAATTCGCGTCCGCTGCTGATACC 394
QY 1014 GAGATAACTGCAAAATCGCAATTCAAATAGACGCTGTTGAGTAAGGAAAGATTGCTGTGCTG 1073
Db 393 GAGATAACTGCAAAATCGCAATTCAAATAGACGCTGTTGAGTAAGGAAAGATTGCTGTGCTG 334
QY 1074 TTCTTCGAGGTTAAATCGGCGCAGGCGAGTCAGCGATCTCCGCAAAATGAGCGGCGCGCT 1133
Db 333 TTCTTCGAGGTTAAATCGGCGCAGGCGAGTCAGCGATCTCCGCAAAATGAGCGGCGCGCT 274
QY 1134 GTAGTTGAATTCAGTGGCGCGGCTTTCCGCCAATCGGTCCGCTCGATCAGCGT 1193
Db 273 GTAGTTGAATTCAGTGGCGCGGCTTTCCGCCAATCGGTCCGCTCGATCAGCGT 214
QY 1194 CTCAGGTATCTTTTGTATGGAACCGTCCCTTTCACCTGGAGCGGAAACAGTTTATCCACTGTAA 1253
Db 213 CTCAGGTATCTTTTGTATGGAACCGTCCCTTTCACCTGGAGCGGAAACAGTTTATCCACTGTAA 154

QY 1254 CCCCTGGCTCGTTTGTATCGAATTCGTGTTTCGCCAATACAGTCTGGTATATTGCAATGTC 1313
DB 153 CCCCTGGCTCGTTTGTATCGAATTCGTGTTTCGCCAATACAGTCTGGTATATTGCAATGTC 94
QY 1314 ATCATAGATGATGAATTCATCGAGCAATGCAATCAGGTCAAAATATCTCGCCAAAGGTAT 1373
DB 93 ATCATAGATGATGAATTCATCGAGCAATGCAATCAGGTCAAAATATCTCGCCAAAGGTAT 34
QY 1374 GTAATTTGATTGAACAATCGGACTTCTTCTCAA 1406
DB 33 GTAATTTGATTGAACAATCGGACTTCTTCTCAA 1

RESULT 3

US-10-388-902-44/c
; Sequence 44, Application US/10388902
; Publication No. US20040018574A1
; GENERAL INFORMATION:
; APPLICANT: Behr, Marcel
; APPLICANT: Schoolnik, Gary
; APPLICANT: Wilson, Michael A.
; TITLE OF INVENTION: Molecular Differences Between Species of
; FILE REFERENCE: STAN102CON
; CURRENT APPLICATION NUMBER: US/10/388,902
; PRIOR FILING DATE: 2003-03-14
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: US/09/894,844
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 60/097,936
; PRIOR FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; TYPE: DNA
; ORGANISM: Mycobacteria tuberculosis
US-10-388-902-44

Query Match 49.3%; Score 693; DB 7; Length 693;
Best Local Similarity 100.0%; Pred. No. 3.7e-227;
Matches 693; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 714 CTGGCGACAGTACCTCAATAGTCCGAGGCTCGGCTCCGACGTTTAAAGAGCAGATCCAG 773
DB 693 CTGGCGACAGTACCTCAATAGTCCGAGGCTCGGCTCCGACGTTTAAAGAGCAGATCCAG 634
QY 774 AATCGACACGGGGCTCGAACCCTCCCAATTCGTTTATATCGCGGTAGCCGTCATA 833
DB 633 AATCGACACGGGGCTCGAACCCTCCCAATTCGTTTATATCGCGGTAGCCGTCATA 574
QY 834 ATCGAACCAAGTTACCCGGATGTAAGTTGTCGAACACGCGCTCATCGACATACGAACG 893
DB 573 ATCGAACCAAGTTACCCGGATGTAAGTTGTCGAACACGCGCTCATCGACATACGAACG 514
QY 894 GGTGAGGGGCCAGACACATATTCGTCGTCGGGCTGTTGGCAGAGGTTGGCCAGTCT 953
DB 513 GGTGAGGGGCCAGACACATATTCGTCGTCGGGCTGTTGGCAGAGGTTGGCCAGTCT 454
QY 954 CTCGGTCTTGGCTCGGCTCAATTCGTCGTCGCAAGTATTCGCGTCTGCTGATACC 1013
DB 453 CTCGGTCTTGGCTCGGCTCAATTCGTCGTCGCAAGTATTCGCGTCTGCTGATACC 394
QY 1014 GAGATAACTGCAATCGCATTCATAGACGCTGTTGAGTAAGAAAGATTTCGTGTGCTG 1073
DB 393 GAGATAACTGCAATCGCATTCATAGACGCTGTTGAGTAAGAAAGATTTCGTGTGCTG 334
QY 1074 TTCCTCGAGGTAATCGGCGCGAGCCAGTCAGCGATCTCCGCAAAATAGCGGCGCGCT 1133
DB 333 TTCCTCGAGGTAATCGGCGCGAGCCAGTCAGCGATCTCCGCAAAATAGCGGCGCGCT 274

QY 1134 GTAGTTGAATTTAGTGGCCCGCAGTGCCTTTTCGCCAATCGGTCCCGTCGATCAGCGT 1193
DB 273 GTAGTTGAATTTAGTGGCCCGCAGTGCCTTTTCGCCAATCGGTCCCGTCGATCAGCGT 214
QY 1194 CTCACGTATCTTTTGTATGGAACGTCCTTTCACCTGGACGGGACAGTTTATCCACTGTAA 1253
DB 213 CTCACGTATCTTTTGTATGGAACGTCCTTTCACCTGGACGGGACAGTTTATCCACTGTAA 154
QY 1254 CCCCTGGCTCGTTTGTATCGGATTTCTGTTTCGCCAATCAGCTTCGTTGGTATATTGCAATGTC 1313
DB 153 CCCCTGGCTCGTTTGTATCGGATTTCTGTTTCGCCAATCAGCTTCGTTGGTATATTGCAATGTC 94
QY 1314 ATCATAGATGATGAATTCATCGAGCAATGCAATCAGGTCAAAATATCTCGCCAAAGGTAT 1373
DB 93 ATCATAGATGATGAATTCATCGAGCAATGCAATCAGGTCAAAATATCTCGCCAAAGGTAT 34
QY 1374 GTAATTTGATTGAACAATCGGACTTCTTCTCAA 1406
DB 33 GTAATTTGATTGAACAATCGGACTTCTTCTCAA 1

RESULT 4

US-10-647-089-44/c
; Sequence 44, Application US/10647089
; Publication No. US20040063923A1
; GENERAL INFORMATION:
; APPLICANT: Behr, Marcel
; APPLICANT: Small, Peter
; APPLICANT: Schoolnik, Gary
; APPLICANT: Wilson, Michael A.
; TITLE OF INVENTION: Molecular Differences Between Species of
; FILE REFERENCE: STAN102CON
; CURRENT APPLICATION NUMBER: US/10/647,089
; PRIOR FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: US/09/894,844
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/318,191
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 60/097,936
; PRIOR FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 693
; TYPE: DNA
; ORGANISM: Mycobacteria tuberculosis
US-10-647-089-44

Query Match 49.3%; Score 693; DB 7; Length 693;
Best Local Similarity 100.0%; Pred. No. 3.7e-227;
Matches 693; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 714 CTGGCGACAGTACCTCAATAGTCCGAGGCTCGGCTCCGACGTTTAAAGAGCAGATCCAG 773
DB 693 CTGGCGACAGTACCTCAATAGTCCGAGGCTCGGCTCCGACGTTTAAAGAGCAGATCCAG 634
QY 774 AATCGACACGGGGCTCGAACCCTCCCAATTCGTTTATATCGCGGTAGCCGTCATA 833
DB 633 AATCGACACGGGGCTCGAACCCTCCCAATTCGTTTATATCGCGGTAGCCGTCATA 574
QY 834 ATCGAACCAAGTTACCCGGATGTAAGTTGTCGAACACGCGCTCATCGACATACGAACG 893
DB 573 ATCGAACCAAGTTACCCGGATGTAAGTTGTCGAACACGCGCTCATCGACATACGAACG 514
QY 894 GGTGAGGGGCCAGACACATATTCGTCGTCGGGCTGTTGGCAGAGGTTGGCCAGTCT 953
DB 513 GGTGAGGGGCCAGACACATATTCGTCGTCGGGCTGTTGGCAGAGGTTGGCCAGTCT 454
QY 954 CTCGGTCTTGGCTCGGCTCAATTCGTCGTCGCAAGTATTCGCGTCTGCTGATACC 1013
DB 453 CTCGGTCTTGGCTCGGCTCAATTCGTCGTCGCAAGTATTCGCGTCTGCTGATACC 394

1014 GAGATAACTGCAATCGCATTCATATAGACGCTGTTGAGTAAGGAAGGATTCGTGTGCTG 1073
|||||
393 GAGATAACTGCAATCGCATTCATATAGACGCTGTTGAGTAAGGAAGGATTCGTGTGCTG 334
|||||
1074 TTCTTCGAGGTAATCGGCGGAGCGAGTCAGCGATCTCCGCAAAATGAGCGCGCGCT 1133
333 TTCTTCGAGGTAATCGGCGGAGCGAGTCAGCGATCTCCGCAAAATGAGCGCGCGCT 274
|||||
1134 GTAGTTGAATTCAGTGCCTGCGCGAGTCGGTTCGCGCAATCGGTGCCCTCGATCAGCGT 1193
Db GTAGTTGAATTCAGTGCCTGCGCGAGTCGGTTCGCGCAATCGGTGCCCTCGATCAGCGT 214
|||||
1194 CTCACGTATCTTTGATGGAAGCTCCCTTCACCTGAGCGGAACAGTTATCCACTGTAA 1253
Db CTCACGTATCTTTGATGGAAGCTCCCTTCACCTGAGCGGAACAGTTATCCACTGTAA 154
|||||
1254 CCCCTGGCTCGTTTGGATCGGATTTCTGTTTGGCCCAATCAGCTTGGTATATTTGCATGTC 1313
Db CCCCTGGCTCGTTTGGATCGGATTTCTGTTTGGCCCAATCAGCTTGGTATATTTGCATGTC 94
|||||
1314 ATCATAGATGATGAATTCATTCGACGAATGCAATCAGGTCAAAATATCTTCGCAAGGTAT 1373
Db ATCATAGATGATGAATTCATTCGACGAATGCAATCAGGTCAAAATATCTTCGCAAGGTAT 34
|||||
1374 GTAATTTGATTCGAACAATCGGACTTTCTTCAA 1406
Db GTAATTTGATTCGAACAATCGGACTTTCTTCAA 1

RESULT 5

US-09-894-844-43/c
; Sequence 43, Application US/09894844
; Patent No. US20020176873A1
; GENERAL INFORMATION:
; APPLICANT: Behr, Marcel
; APPLICANT: Small, Peter
; APPLICANT: Schoolnik, Gary
; APPLICANT: Wilson, Michael A.
; TITLE OF INVENTION: Molecular Differences Between Species of
; FILE REFERENCE: STAN102CON
; CURRENT APPLICATION NUMBER: US/09/894,844
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/318,191
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 60/097,936
; PRIOR FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 498
; TYPE: DNA
; ORGANISM: Mycobacteria tuberculosis
US-09-894-844-43

Query Match 30.3%; Score 427; DB 3; Length 498;
Best Local Similarity 100.0%; Pred. No. 1.3e-135;
Matches 427; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACCTGCGCTTCAGAGATCAATAGGCGCATGGGTTCAGCATAGTACAGGTTCGTGCGCA 60
Db 427 ACCTGCGCTTCAGAGATCAATAGGCGCATGGGTTCAGCATAGTACAGGTTCGTGCGCA 368
|||||
QY 61 TCTTTGATGATCGGAAATAGATGTGAGGCAATTTAAAGAGAGCGCACCGGACTTCGCGG 120
Db 367 TCTTTGATGATCGGAAATAGATGTGAGGCAATTTAAAGAGAGCGCACCGGACTTCGCGG 308
|||||
QY 121 CATTCAGCATGTCGAGCGTCGCTTCGATGTAGCGGACCAATTCGCGTGTCCACGATTTCA 180
Db 307 CATTCAGCATGTCGAGCGTCGCTTCGATGTAGCGGACCAATTCGCGTGTCCACGATTTCA 248
|||||
QY 181 GACGAACATTGAATTTCCACTTCGCGACGCTATAGTCCGCTCCCGATCTATGCGCGCG 240

Db 247 GACGAACATTGAATTTCCACTTCGCGACGCTATAGTCCGCTCCCGATCTATGCGCGCG 188
QY 241 CGCAGATGAAGTCTCGGTTTCGCCGACCTTCGAAACAGTAGTCGGCGCGCGCACCATTT 300
|||||
Db 187 CGCAGATGAAGTCTCGGTTTCGCCGACCTTCGAAACAGTAGTCGGCGCGCGCACCATTT 128
QY 301 CGGGGAGACGTCGATGCGGCTGTAATCAGTTTTCGAAGCCACGCGCATCTAGGTAGTCCA 360
Db 127 CGGGGAGACGTCGATGCGGCTGTAATCAGTTTTCGAAGCCACGCGCATCTAGGTAGTCCA 68
QY 361 GTAGAGCCCCATAGCACACAGCCTAGATCGTTTCGAAAAATGGTCCGCGCAATTGACAA 420
Db 67 GTAGAGCCCCATAGCACACAGCCTAGATCGTTTCGAAAAATGGTCCGCGCAATTGACAA 8
QY 421 TCGGCAC 427
|||||
Db 7 TCGGCAC 1

RESULT 6

US-10-388-902-43/c
; Sequence 43, Application US/10388902
; Publication No. US20040018574A1
; GENERAL INFORMATION:
; APPLICANT: Behr, Marcel
; APPLICANT: Small, Peter
; APPLICANT: Schoolnik, Gary
; APPLICANT: Wilson, Michael A.
; TITLE OF INVENTION: Molecular Differences Between Species of
; FILE REFERENCE: STAN102CON
; CURRENT APPLICATION NUMBER: US/10/388,902
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: US/09/894,844
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/318,191
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 60/097,936
; PRIOR FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 498
; TYPE: DNA
; ORGANISM: Mycobacteria tuberculosis
US-10-388-902-43

Query Match 30.3%; Score 427; DB 7; Length 498;
Best Local Similarity 100.0%; Pred. No. 1.3e-135;
Matches 427; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACCTGCGCTTCAGAGATCAATAGGCGCATGGGTTCAGCATAGTACAGGTTCGTGCGCA 60
Db 427 ACCTGCGCTTCAGAGATCAATAGGCGCATGGGTTCAGCATAGTACAGGTTCGTGCGCA 368
|||||
QY 61 TCTTTGATGATCGGAAATAGATGTGAGGCAATTTAAAGAGAGCGCACCGGACTTCGCGG 120
Db 367 TCTTTGATGATCGGAAATAGATGTGAGGCAATTTAAAGAGAGCGCACCGGACTTCGCGG 308
|||||
QY 121 CATTCAGCATGTCGAGCGTCGCTTCGATGTAGCGGACCAATTCGCGTGTCCACGATTTCA 180
Db 307 CATTCAGCATGTCGAGCGTCGCTTCGATGTAGCGGACCAATTCGCGTGTCCACGATTTCA 248
|||||
QY 181 GACGAACATTGAATTTCCACTTCGCGACGCTATAGTCCGCTCCCGATCTATGCGCGCG 240
Db 247 GACGAACATTGAATTTCCACTTCGCGACGCTATAGTCCGCTCCCGATCTATGCGCGCG 188
QY 241 CGCAGATGAAGTCTCGGTTTCGCCGACCTTCGAAACAGTAGTCGGCGCGCGCACCATTT 300
Db 187 CGCAGATGAAGTCTCGGTTTCGCCGACCTTCGAAACAGTAGTCGGCGCGCGCACCATTT 128
QY 301 CGGGGAGACGTCGATGCGGCTGTAATCAGTTTTCGAAGCCACGCGCATCTAGGTAGTCCA 360
|||||

Db 127 CGGGGAGACGTGATCGCCGGTGTAAATCAGTTTTTGAAGCCACGCGCATCTAGGTAGTCCA 68
QY 361 GTAGAGCCCATAGCCACACCTAGATCGTTGATCGAAATGGTCCGCGCATTCACAA 420
Db 67 GTAGAGCCCATAGCCACACCTAGATCGTTGATCGAAATGGTCCGCGCATTCACAA 8
QY 421 TGGGCAC 427
Db 7 TGGGCAC 1

RESULT 7
US-10-647-089-43/c
; Sequence 43, Application US/10647089
; Publication No. US20040063923A1
; GENERAL INFORMATION:
; APPLICANT: Behr, Marcel
; APPLICANT: Small, Peter
; APPLICANT: Schoolnik, Gary
; APPLICANT: Wilson, Michael A.
; TITLE OF INVENTION: Molecular Differences Between Species of
; FILE REFERENCE: the M. Tuberculosis Complex
; CURRENT APPLICATION NUMBER: US/10/647,089
; PRIOR FILING DATE: 2003-08-21
; PRIOR FILING DATE: 2001-06-27
; PRIOR FILING DATE: 1999-05-25
; PRIOR FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 498
; TYPE: DNA
; ORGANISM: Mycobacteria tuberculosis
US-10-647-089-43

Query Match 30.3%; Score 427; DB 7; Length 498;
Best Local Similarity 100.0%; Pred. No. 1.3e-135;
Matches 427; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACCTGCGCTTGACAGATCAATAGGCGCATGGTGCAGCATAGTACAGTCTGTCGCGCA 60
Db 427 ACCTGCGCTTGACAGATCAATAGGCGCATGGTGCAGCATAGTACAGTCTGTCGCGCA 368
QY 61 TCTTTGATGATCGGAATAGATGTGAGGCAATTTAAAGAGAGCCACGCGACTCGCGG 120
Db 367 TCTTTGATGATCGGAATAGATGTGAGGCAATTTAAAGAGAGCCACGCGACTCGCGG 308
QY 121 CATTCAGCATGTGAGGCGTTCGATGTGAGGCGCACCATTCGTTGTCACAGATTCA 180
Db 307 CATTCAGCATGTGAGGCGTTCGATGTGAGGCGCACCATTCGTTGTCACAGATTCA 248
QY 181 GAGCAATTTGAATATTCACCTCGGCGCATGTAGTCCGCTCCGCTCTATGCGCGCG 240
Db 247 GAGCAATTTGAATATTCACCTCGGCGCATGTAGTCCGCTCCGCTCTATGCGCGCG 188
QY 241 CGCAGATGAAGTCTGCGTTTCGCGCGCATTCGAAACGTTAGTGGCGCGCGCGCACCATTT 300
Db 187 CGCAGATGAAGTCTGCGTTTCGCGCGCATTCGAAACGTTAGTGGCGCGCGCGCACCATTT 128
QY 301 CGGGGAGAGCTGATGCGCGGTGTAATCAGTTTTTGAAGCCACGCGCATCTAGGTAGTCCA 360
Db 127 CGGGGAGAGCTGATGCGCGGTGTAATCAGTTTTTGAAGCCACGCGCATCTAGGTAGTCCA 68
QY 361 GTAGAGCCCATAGCCACACCTAGATCGTTGATCGAAATGGTCCGCGCATTCACAA 420
Db 67 GTAGAGCCCATAGCCACACCTAGATCGTTGATCGAAATGGTCCGCGCATTCACAA 8
QY 421 TGGGCAC 427
Db 7 TGGGCAC 1

Db 7 TGGGCAC 1

RESULT 8
US-10-087-192-1528
; Sequence 1528, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1528
; LENGTH: 27204
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-087-192-1528

Query Match 2.8%; Score 39.8; DB 5; Length 27204;
Best Local Similarity 48.1%; Pred. No. 0.24;
Matches 113; Conservative 0; Mismatches 122; Indels 0; Gaps 0;

QY 411 GCATTGACAATGCGCACACGAGTGTGTCACAAAGCGCAAGCTTGCCTGCGCGCTTCGCGCTTCCAA 470
Db 19391 GCCTAGGGCTTGGCGAGCTGTGACCAAGCGGGGCCACCTTGCCTGCTGTAGCCCTTCCAG 19450
QY 471 TCGACGCGCGCGGTGCGGTGCTTTCGAGTTTCGATGCTAGTAACGCGGCCACGCTCAG 530
Db 19451 GTGACGCGCGAGCCAGAGCCCTGGCGTGGAGGTGAGTGGCAGCAGAGGGCTGTGTGAG 19510
QY 531 CGAGCATGCTGCTTGGCTTTCGCGCATGAGTGTGCTCAGATTGTTGTGTGTGGCGGT 590
Db 19511 AGTGGCTGTTTCTCCACAGCTGACTTTGGGGTGTGAGGCGAGCTGACAGCGTCTGTGG 19570
QY 591 CGGTGCGTGGTCCGAGACTATACCTTCAACAGTTTCATGCTGCGAGGCTGCGGCGG 645
Db 19571 CCAGAGGAGGTCTTTCATTTGGGACTCCCTACTGTTGAGGCTGCGCTGCGGCGG 19625

RESULT 9
US-10-521-103-1
; Sequence 1, Application US/10521103
; Publication No. US20050136071A1
; GENERAL INFORMATION:
; APPLICANT: Griffiths, Steven Gareth
; APPLICANT: Ritchie, Rachel Jane
; APPLICANT: Simard, Nathalie C.
; TITLE OF INVENTION: Hsp70 from Arthrobacter
; FILE REFERENCE: H-32534-A
; CURRENT APPLICATION NUMBER: US/10/521,103
; CURRENT FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: PCT/EP03/07602
; PRIOR FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: GB 0216414.3
; PRIOR FILING DATE: 2002-07-15
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2464
; TYPE: DNA
; ORGANISM: Arthrobacter
US-10-521-103-1

Query Match 2.7%; Score 38.4; DB 9; Length 2464;

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Best Local Similarity 48.6%; Pred. No. 0.22;
Matches 105; Conservative 0; Mismatches 111; Indels 0; Gaps 0;

QY 205 CGACGCTATAGTCGGCTCCGATCTATCGCGCGCGCAGATGAAGTCTGCTTGGCCC 264
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 515 CGACTGGACCGTCGGCATCGACACAAGATACACCGCGCAGGAATCTCGCGCGCAC 574
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 265 GACCTTCGAAAGTATGTCGGCGCGCGCACCATTTCCGGGGGAGAGCTGATCCGGTGT 324
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 575 CTTGATGAAGCTCAAGAACGACGCCGAGTCTTCTTGGCGGAAAGGTCACCGACGCGT 634
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 325 AATCAGTTTGAAGCCACGCGATCTAGGTAGTCCAGTAGAGCCCATAGCCACAGCCCTA 384
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 635 GATCAGGTTCTGCTACTTTCAAGACCGCGAGCGCCAGGCCACCAAGAAGCCGGTGA 694
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 385 GATCGTTGATGAAATGGTCCGCGCATTGACAA 420
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 695 GATCGCGCGCTGAACGTCTGCGCATCGTCAACGA 730
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 10
US-10-338-110-119/c
; Sequence 119, Application US/10338110
; Publication No. US20040023254A1
; GENERAL INFORMATION:
; APPLICANT: Fuhrmann, Jeffrey J.
; APPLICANT: Romesser, James A.
; TITLE OF INVENTION: A Method To Assess Quorum Sensing Potential of Microbial
; FILE OF INVENTION: Communities
; CURRENT APPLICATION NUMBER: US/10/338,110
; CURRENT FILING DATE: 2003-01-07
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 119
; LENGTH: 536
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (7)..(7)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (21)..(21)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (33)..(33)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (69)..(69)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (87)..(87)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (213)..(213)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (226)..(226)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (261)..(261)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
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; NAME/KEY: misc feature
; LOCATION: (273)..(273)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (347)..(347)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (357)..(357)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (398)..(398)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (419)..(419)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (517)..(517)
; OTHER INFORMATION: n is a, c, g, or t
US-10-338-110-119

Query Match 2.7%; Score 37.8; DB 7; Length 536;
Best Local Similarity 10.0%; Pred. No. 0.16;
Matches 33; Conservative 170; Mismatches 128; Indels 0; Gaps 0;

QY 290 GCGCACCATTTTCGGGGGAGACGTCGATCGCGGTGTAATCAGTTTGAAGCCACGCGCATC 349
    :||: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 536 KCAEMRVYHCBVMBKVBVCVVDYBGRDKSSVRRMGSMRVDBSKYBRBGSHKYG 477
    :||: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 350 TAGGTAGTCCAGTAGAGCCCATAGCCACAGCCTAGATCGTTGATCGAAAAATGGTCCGC 409
    : : : : ||||: : : : : : : : : : : : : : : : : : : : : : : : : :
Db 476 HTVBYGRTCCRSASGCSASSABYDKHYBVVYVDWBSDDKVRSCGRVCCRSBCGNTS 417
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 410 CGCATTGACAATGCGCACCGACGCTGTCAAAGCGCAACGCGCTCGCCGCTTCGCCGTCCA 469
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 416 SDVSHKBAVCCGWTSMKNHBGMWRSCBWCCTATSSVYVGDWSRYSPRSCSAYSAN 357
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 470 ATCGACGCGCGCGGTGCGTGTGCTTCGAGTTTCGATGCGTAGTAACGGGCGCAGTCA 529
    : : : : ||||: : : : : : : : : : : : : : : : : : : : : : : : : :
Db 356 SBVMYBBGCNCCSVBWRSSHGCKSWYTBSSASGVYKBHSSMSARAYMBKCAYSGCCMR 297
    : : : : ||||: : : : : : : : : : : : : : : : : : : : : : : : : :

QY 530 GCGACATGGTGTGCTGCTTCGCCCATGAAGCTGCCTCAGATTGTGTGTGGGCG 589
    : : : : ||||: : : : : : : : : : : : : : : : : : : : : : : : : :
Db 296 KTSGSDYGYGKGYGWAACGNGMADYTCCCANAYSKMBGATBSBKSOGYRKKBYB 237
    : : : : ||||: : : : : : : : : : : : : : : : : : : : : : : : : :

QY 590 TCGGTGCGTGGTCCGAGACTATACCTCAA 620
    : : : : ||||: : : : : : : : : : : : : : : : : : : : : : : : : :
Db 236 YSBVGMVSRNRKVSRYRAABASNBMYTVA 206
    : : : : ||||: : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 11
US-10-156-761-1933/c
; Sequence 1933, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
```

; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1933
; LENGTH: 894
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(894)
US-10-156-761-1933

Query Match 2.7%; Score 37.8; DB 6; Length 894;
Best Local Similarity 61.9%; Pred. No. 0.21; 37; Indels 0; Gaps 0;
Matches 60; Conservative 0; Mismatches 37; Indels 0; Gaps 0;
QY 403 GGTCCCGCCGATTCACAAATGCGCAGCTGGTCAAAAGCGCAACGCTGCCGGCTTCGC 462
DB 192 GGCCGACTCGCGGAGACGACCAAGTTGGCCCGCCACAGGCGCGCGGCTTCGT 133
QY 463 CGTTCCAATCGACGCGCGCGGTGCGGTGCTTCG 499
DB 132 CGTCGGCTTCGTGTCGCGCGGTGATCGGGTCTCG 96

RESULT 12

US-10-156-761-1
; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1

Query Match 2.7%; Score 37.8; DB 6; Length 9025608;
Best Local Similarity 61.9%; Pred. No. 22;
Matches 60; Conservative 0; Mismatches 37; Indels 0; Gaps 0;
QY 403 GGTCCCGCCGATTCACAAATGCGCAGCTGGTCAAAAGCGCAACGCTGCCGGCTTCGC 462
DB 2380428 GGCCGACTCGCGGAGACGACCAAGTTGGCCCGCCACAGGCGCGCGGCTTCGT 2380487
QY 463 CGTTCCAATCGACGCGCGGTGCGGTGCTTCG 499
DB 2380488 CGTCGGCTTCGTGTCGCGCGGTGATCGGGTCTCG 2380524

RESULT 13

US-10-437-963-48583
; Sequence 48583, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(51221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 48583
; LENGTH: 485
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(485)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_51244C.1
US-10-437-963-48583

Query Match 2.6%; Score 36.6; DB 7; Length 485;
Best Local Similarity 43.8%; Pred. No. 0.41;
Matches 156; Conservative 0; Mismatches 200; Indels 0; Gaps 0;
QY 241 CCAGATGAAGTCTCGTTGCGCCGACCTTTCGAAAGCTAGTGTGCGCGCGCACCATTT 300
DB 85 CTCTCGAGTTGACAGCATCTGAAAGCTTCTCATGCAAGTGGATGCTTTACTTTATTA 144
QY 301 CGGGGAGAGCTCGATGCGGTGTAATCAGTTTGAAGCCAGCGCATCTAGTGTCTCCA 360
DB 145 TTCATCAGTACAGTACATTTGTTGATCATATTTGTTCTCTCAGTCTCTCAAGGAATGAA 204
QY 361 GTAGAGCCCATAGCCACAGCCTAGATCGTTGATCGAAATGGTCCGCGCATTCACAA 420
DB 205 GGATACCAGCACAGAGAACAAATTTATTCATCCAGACATGGCATCAAGGAAGCAAC 264
QY 421 TCGGCACAGCTGGTCAAGCGCAACGCTGCCGCTTTCGCGGTTTCCAAATCGACCGCG 480
DB 265 TCATCACAATCTACACTAACTCCACGCTTACTCTTCTTCGTGAGAAACCTTCTCGGCT 324
QY 481 GCGGTGCGGTGCTTTCGAGTTTCGATCGTAGTAACGCGCCACGTCAGCGCATGTGT 540
DB 325 GAACGCGCGAGATCGACGATCTTGGCATCGCGCTCGAGGATGAGCTCTGCGAGAGCGGC 384
QY 541 CGTTGCTCTCCGCCATGAAGCTGCTCAGCATTTGTGTGTGGCGCTTCGCTGC 596
DB 385 ACCGTGGCTGAGCATTTGAGGATCCCCCAGCAGCTGTCCCGGCGGACATAGC 440

RESULT 14

US-10-156-761-2972/c
; Sequence 2972, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 20, 2006, 01:43:06 ; Search time 459.429 Seconds
(without alignments)
6500.886 Million cell updates/sec

Title: US-09-673-476-1_COPY_1_1407

Perfect score: 1407

Sequence: 1 acctgcgttgagatca.....caatcgagctttcttcaac 1407

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 7204252 seqs, 106136211 residues

Total number of hits satisfying chosen parameters: 14408504

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA New:*

- 1: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1407	100.0	12732	8	US-10-802-796-1
2	693	49.3	693	12	US-11-143-401-44
3	427	30.3	498	12	US-11-143-401-43
4	36.2	2.6	88116	8	US-10-995-561-13351
5	36.2	2.6	222094	8	US-10-995-561-13244
6	35.4	2.5	622	6	US-09-925-065A-597843
7	34.6	2.5	388	6	US-09-925-065A-585977
8	34.6	2.5	496	6	US-09-925-065A-827710
9	34.2	2.4	634	6	US-09-925-065A-311017
10	33.8	2.4	810	8	US-10-467-657-5805
11	33.6	2.4	535	6	US-09-925-065A-288675
12	33.4	2.4	388	6	US-09-925-065A-585978
13	33.4	2.4	613	6	US-09-925-065A-411236
14	33.4	2.4	1194	6	US-09-925-065A-279367
15	33.2	2.4	600	8	US-10-750-185-707
16	33.2	2.4	600	8	US-10-750-623-707
17	33	2.3	388	6	US-09-925-065A-585976
18	33	2.3	634	6	US-09-925-065A-311018
19	33	2.3	634	6	US-09-925-065A-311019
20	32.6	2.3	164810	12	US-11-121-086-4

21	32.4	2.3	568	6	US-09-925-065A-649740	Sequence 649740,	
22	32.4	2.3	623	6	US-09-925-065A-839523	Sequence 839523,	
23	32.2	2.3	636	6	US-09-925-065A-328950	Sequence 328950,	
24	32	2.3	568	6	US-09-925-065A-649739	Sequence 649739,	
25	31.8	2.3	518	6	US-09-925-065A-737967	Sequence 737967,	
26	31.8	2.3	636	6	US-09-925-065A-328949	Sequence 328949,	
c	27	31.8	2.3	2157	8	US-10-467-657-761	Sequence 761, App
c	28	31.8	2.3	2319	8	US-10-858-730-148	Sequence 148, App
c	29	31.8	2.3	159695	12	US-11-121-086-56	Sequence 56, Appl
c	30	31.6	2.2	158692	12	US-11-121-086-30	Sequence 30, Appl
31	31.4	2.2	611	6	US-09-925-065A-482107	Sequence 482107,	
c	32	31.4	2.2	1020	8	US-10-467-657-7407	Sequence 7407, Ap
c	33	31.4	2.2	1020	8	US-10-467-657-8249	Sequence 8249, Ap
c	34	31.4	2.2	1085	8	US-10-683-512-131	Sequence 131, App
c	35	31.4	2.2	1398	8	US-10-750-185-24726	Sequence 24726, A
c	36	31.4	2.2	1398	8	US-10-750-623-24726	Sequence 24726, A
c	37	31.2	2.2	596	6	US-09-925-065A-813872	Sequence 813872,
c	38	31.2	2.2	165857	12	US-11-121-086-34	Sequence 34, Appl
c	39	31	2.2	629	6	US-09-925-065A-695006	Sequence 695006,
c	40	31	2.2	654	6	US-09-925-065A-630116	Sequence 630116,
c	41	31	2.2	1485	8	US-10-750-185-40943	Sequence 40943, A
c	42	31	2.2	1485	8	US-10-750-623-40943	Sequence 40943, A
c	43	30.8	2.2	317	12	US-11-043-752-2163	Sequence 2163, Ap
c	44	30.8	2.2	612	6	US-09-925-065A-790506	Sequence 790506,
c	45	30.8	2.2	94905	12	US-11-117-187-208	Sequence 208, App

ALIGNMENTS

RESULT 1

US-10-802-796-1
; Sequence 1, Application US/10802796
; Publication No. US20050250104A1
; GENERAL INFORMATION:
; APPLICANT: COLE, STEWART
; APPLICANT: BUCHRIER-BROSCH, ROLAND
; APPLICANT: GORDON, STEPHEN
; APPLICANT: BILLAULT, ALAIN
; TITLE OF INVENTION: A METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST
; TITLE OF INVENTION: FROM THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED
; TITLE OF INVENTION: DNA LIBRARY. APPLICATION TO THE DETECTION OF
; TITLE OF INVENTION: MYCOBACTERIA.
; FILE REFERENCE: 05394.0011-00000
; CURRENT APPLICATION NUMBER: US/10/802,796
; PRIOR FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: US/09/673,476
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: PCT/IB99/00740
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 09/060,756
; PRIOR FILING DATE: 1998-04-16
; NUMBER OF SEQ ID NOS: 743
; SOFTWARE: PatentIn Ver. 2.2
; SEQ ID NO 1
; LENGTH: 12732
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-10-802-796-1

Query Match	100.0%;	Score 1407;	DB 8;	Length 12732;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1407;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ACCTCGCTTGAGAGATCAAAATAGCGGCATGGGTGACATAGTACAGTTCGTCGCGCA	60	
Db	1	ACCTCGCTTGAGAGATCAAAATAGCGGCATGGGTGACATAGTACAGTTCGTCGCGCA	60	
QY	61	TCTTTGATCATCGGAATAAGATGTGAGCAATTAAGAGAGCCAGCGGACTCGCGG	120	
Db	61	TCTTTGATCATCGGAATAAGATGTGAGCAATTAAGAGAGCCAGCGGACTCGCGG	120	
QY	121	CATTGAGCATGCGAGCGTCGCTTCGATGTGAGCGCACCATTTCCGTCGTCACAGATTCA	180	

Db 121 CATTGAGATGTCGAGGTCGCTTCGATGTGAGCGCACCATTCCTCGGTCCACGATTTCA 180
QY 181 GACGAACATGTAATATTCACATCGGACGCTATAGTCGCGCTCCGATCTATGCGCGCG 240
Db 181 GACGAACATGTAATATTCACATCGGACGCTATAGTCGCGCTCCGATCTATGCGCGCG 240
QY 241 CGCAGATGAAGTCTGCTTTCGCGGACCTTCGAAAGTAGTGGCGCGCGGACCAATTT 300
Db 241 CGCAGATGAAGTCTGCTTTCGCGGACCTTCGAAAGTAGTGGCGCGCGGACCAATTT 300
QY 301 CGGGGAGACGTCGATCGCGGTGTAATCAGTTTGAAGCCACGCGCATCTAGTAGTCCA 360
Db 301 CGGGGAGACGTCGATCGCGGTGTAATCAGTTTGAAGCCACGCGCATCTAGTAGTCCA 360
QY 361 GTAGAGCCCATAGCCACAGCCTAGATCGTTCGAAATGGTCCGCGCATTTGACAA 420
Db 361 GTAGAGCCCATAGCCACAGCCTAGATCGTTCGAAATGGTCCGCGCATTTGACAA 420
QY 421 TCGGCACAGCTGCTCAAGAGCGGACGCTTCGCGGCTTCGCGGTTCGAAATCGACGCGC 480
Db 421 TCGGCACAGCTGCTCAAGAGCGGACGCTTCGCGGCTTCGCGGTTCGAAATCGACGCGC 480
QY 481 GCGGTGCGCTGCTTTCGAGTTTCGATCGTAGTAAACGGGCCACGTCAGCGAGCATGT 540
Db 481 GCGGTGCGCTGCTTTCGAGTTTCGATCGTAGTAAACGGGCCACGTCAGCGAGCATGT 540
QY 541 CGTTGCGCTTCGCGCATGAAGCTGCTCACGATTTGTGTGTGGCGCTCGGTGCGTGG 600
Db 541 CGTTGCGCTTCGCGCATGAAGCTGCTCACGATTTGTGTGTGGCGCTCGGTGCGTGG 600
QY 601 GTCCGAGACTATACCTTCAACAGTTTCGATCGCGAGCTCGCGGGGCAATGACCCAA 660
Db 601 GTCCGAGACTATACCTTCAACAGTTTCGATCGCGAGCTCGCGGGGCAATGACCCAA 660
QY 661 CCGCGCGGACAGCTTCGCGGACGAGCGTAGTGAAGAGATAGATAATTTCACTGGCA 720
Db 661 CCGCGCGGACAGCTTCGCGGACGAGCGTAGTGAAGAGATAGATAATTTCACTGGCA 720
QY 721 CAGTACCTCAAAATAGTCGAGGCTCGGCTCCGACGTTAAAGAGCAGATCCAGAAATCG 780
Db 721 CAGTACCTCAAAATAGTCGAGGCTCGGCTCCGACGTTAAAGAGCAGATCCAGAAATCG 780
QY 781 ACGGGGGCTCGAAACCTCCGACAAATTCGTTATTAATTCGCGGTAGCCGTCATTAATCG 840
Db 781 ACGGGGGCTCGAAACCTCCGACAAATTCGTTATTAATTCGCGGTAGCCGTCATTAATCG 840
QY 841 CAAAGTTACCCGGATGCTAAGTTTCGTCGAACACGCGCTCATCGACATACGAAACGGGCTG 900
Db 841 CAAAGTTACCCGGATGCTAAGTTTCGTCGAACACGCGCTCATCGACATACGAAACGGGCTG 900
QY 901 GGGCCAGAGACATATTCGCTCGCTCGGCTCTGTTGGCAGAGGTTGGCCAGTCTCTCGGTC 960
Db 901 GGGCCAGAGACATATTCGCTCGCTCGGCTCTGTTGGCAGAGGTTGGCCAGTCTCTCGGTC 960
QY 961 TTGCGGTGCGCTAAATTCGTAGTCCGACGAAATTCGCGAGTCGCTGATGATACGAGATAA 1020
Db 961 TTGCGGTGCGCTAAATTCGTAGTCCGACGAAATTCGCGAGTCGCTGATGATACGAGATAA 1020
QY 1021 CTGCAAAATCGCATTCGAATAGACGCTGTTGAGTAAGGAAGATTCGTGTGCTGTTCTCG 1080
Db 1021 CTGCAAAATCGCATTCGAATAGACGCTGTTGAGTAAGGAAGATTCGTGTGCTGTTCTCG 1080
QY 1081 AGGTAAATCGGCGGAGCCAGTCAGCGATCTCCGCAAAATGAGCGCGCGCTGTAGTTG 1140
Db 1081 AGGTAAATCGGCGGAGCCAGTCAGCGATCTCCGCAAAATGAGCGCGCGCTGTAGTTG 1140
QY 1141 AATTCTAGTCCGCGCAGTCGCTTTCGCGCAATTCGGTCCGCTCGATCAGCGTCTCACGT 1200
Db 1141 AATTCTAGTCCGCGCAGTCGCTTTCGCGCAATTCGGTCCGCTCGATCAGCGTCTCACGT 1200
QY 1201 ATCTTTTGTAGTGAACAGCTCCCTTCACCTCGAGCGGAACAGTTATCCACCTGTAAACCCCTCG 1260

Db 1201 ATCTTTTGTAGTGAACAGCTCCCTTCACCTCGAGCGGAACAGTTATCCACCTGTAAACCCCTGG 1260
QY 1261 CTCGTTTTTGTATCCGATTTCTGTTTGGCCAATCACGCTTGGTATATTTGCATGTCATCATAG 1320
Db 1261 CTCGTTTTTGTATCCGATTTCTGTTTGGCCAATCACGCTTGGTATATTTGCATGTCATCATAG 1320
QY 1321 ATGATGAATTCATCGACGAATCAATCAGGTCAAAATATCCTCGCAAGGTATGTAATTT 1380
Db 1321 ATGATGAATTCATCGACGAATCAATCAGGTCAAAATATCCTCGCAAGGTATGTAATTT 1380
QY 1381 GATTGAACAATCGGACTTTCTTCAAC 1407
Db 1381 GATTGAACAATCGGACTTTCTTCAAC 1407

RESULT 2

US-11-143-401-44/c
; Sequence 44, Application US/11143401
; Publication No. US20060002953A1
; GENERAL INFORMATION:
; APPLICANT: Behr, Marcel
; APPLICANT: Small, Peter
; APPLICANT: Schoolnik, Gary
; APPLICANT: Wilson, Michael A.
; TITLE OF INVENTION: Molecular Differences Between Species of
; TITLE OF INVENTION: the M. Tuberculosis Complex
; FILE REFERENCE: STAN102CON
; CURRENT APPLICATION NUMBER: US/11/143,401
; CURRENT FILING DATE: 2005-06-01
; PRIOR APPLICATION NUMBER: US/10/647,089
; PRIOR FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: US/09/894,844
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/318,191
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 60/097,936
; PRIOR FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 693
; TYPE: DNA
; ORGANISM: Mycobacteria tuberculosis
US-11-143-401-44

Query Match 49.3%; Score 693; DB 12; Length 693;
Best Local Similarity 100.0%; Pred. No. 1.6e-211;
Matches 693; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 714 CTGGGACAGTACCTCAAAATAGTCGGAGCCTCGGCTCCGACGCTTAAAGACGATCCAG 773
Db 693 CTGGGACAGTACCTCAAAATAGTCGGAGCCTCGGCTCCGACGCTTAAAGACGATCCAG 634
QY 774 AATCGACACGCGGCTCGAACCTCCGACAAATTCGTTTATTAATCGCGGTAGCCGTCATA 833
Db 633 AATCGACACGCGGCTCGAACCTCCGACAAATTCGTTTATTAATCGCGGTAGCCGTCATA 574
QY 834 ATCGAACCAAGTTACCCGGATGCTAAGTTTCGTAACACGCGCTCATCGACATACGAACG 893
Db 573 ATCGAACCAAGTTACCCGGATGCTAAGTTTCGTAACACGCGCTCATCGACATACGAACG 514
QY 894 GGCTGAGGGCCAGAGACATATTCGTCGCTGGGCTGTTGGCAGAGGTTGGCCAGTCT 953
Db 513 GGCTGAGGGCCAGAGACATATTCGTCGCTGGGCTGTTGGCAGAGGTTGGCCAGTCT 454
QY 954 CTCGGTCTTCGCGTCGGCTAAATTCGTAGTCCCAAGAAATTCGCGCTGCTGATACC 1013
Db 453 CTCGGTCTTCGCGTCGGCTAAATTCGTAGTCCCAAGAAATTCGCGCTGCTGATACC 394
QY 1014 GAGATAACTGCAAAATCGCAATTCAAATAGACGCTGTTGAGTAAGGAAGATTCGTGTGCTG 1073
Db 393 GAGATAACTGCAAAATCGCAATTCAAATAGACGCTGTTGAGTAAGGAAGATTCGTGTGCTG 334


```
Best Local Similarity 62.9%; Pred. No. 4.3; Indels 0; Gaps 0;
Matches 56; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 403 GGTCCGCCCATGACAAATCGCAGCAGTGTGTCAAAGCGCAACGCTGCGCGCTTCGC 462
Db 213061 GTTCTGCAGCATCTCCAATGCCCGCAGCCGCGCAGCCAGCGCGCCGCGAGCGCGC 213002

QY 463 CGTTCCAATCGAGCGCGCGGGTGCGGT 491
Db 213001 CTCTCAAAACCCCTCCGCGCAGGAGCCTT 212973
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RESULT 6

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US-09-925-065A-597843/c
; Sequence 597843, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108927.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 597843
; LENGTH: 622
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-597843
```

```
Query Match 2.5%; Score 35.4; DB 6; Length 622;
Best Local Similarity 49.7%; Pred. No. 0.73; Indels 0; Gaps 0;
Matches 90; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

QY 1202 TCTTTTGATGGAACGTCCTTCACCTGGACGGGAACAGTTATCCACTGTAAACCCCTGGC 1261
Db 619 TCCTGGCTACAGCAGTCCTCCACCTAGCCTCTGAGGTGTGCACTATGATGCTGAC 560

QY 1262 TCGTTTGTATCGATTTCTGTTTCGCCAATCAGCTTGGTATATTGCATGTCATCATAGA 1321
Db 559 TAATGTAAATTTTTTTTTTTTTTTTGTAGAAACAGATTCTCTCCATGTTGCCAGGCTGA 500

QY 1322 TGATGAATTCATCGAGCAATGCAATCAGTCAAAATATCTCGCCAAAGTATGTAATTGG 1381
Db 499 TTTCAAAATCTGGGCTCAAGCAATCTCCACCTTAGCCTCCCAAAAGTGTGGGATTAG 440

QY 1382 A 1382
Db 439 A 439
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RESULT 7

```
US-09-925-065A-585977
; Sequence 585977, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108927.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
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; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 585977
; LENGTH: 388
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-585977
```

```
Query Match 2.5%; Score 34.6; DB 6; Length 388;
Best Local Similarity 49.2%; Pred. No. 1.1; Indels 0; Gaps 0;
Matches 88; Conservative 1; Mismatches 90; Indels 0; Gaps 0;

QY 1075 TCTTCAGGTAATAATCGCGCGCAGCCAGTCAGCGATCTCCGCAAAATGAGCGCGCGCTG 1134
Db 143 TCGCCGTGTCTCATGGAGGAGCCAGTCAGAGGTGATTGAATCATGGGGGTGGTTTC 202

QY 1135 TAGTTGAATTCATAGTCCCGCAGTCGCTTTTCGCCCAATCGGTGCGGTGATCAGCGTC 1194
Db 203 TCGTGTCTTCTCATGATAGYGAGTGAGTTCTCATGAGATCTGATGATTTTATAAGCTAC 262

QY 1195 TCAGGTATCTTTTGATGGAACGTCCTTCACCTGGACGGGAACAGTTATCCACTGAA 1253
Db 263 TGGCAATTTCCCTGCTGCACTTATTCTCTCCCTTTCTTTATAAATTACCCAGTCTGA 321
```

RESULT 8

```
US-09-925-065A-827710
; Sequence 827710, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108927.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 827710
; LENGTH: 496
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-827710
```

```
Query Match 2.5%; Score 34.6; DB 6; Length 496;
Best Local Similarity 53.3%; Pred. No. 1.2; Indels 0; Gaps 0;
Matches 73; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 1209 ATGGAACGTCCTTCACCTGGACGGGAACAGTTATCCACTGTAAACCCCTGGCTCGTTT 1268
Db 89 ATAAGAAGGTAACTTCTGCTGGAAGAGTACCAGTCTCTTTTCTGTCGTCATGGTAT 148

QY 1269 GATCCGATTTCTGTTTCGCCAATCAGCTTGGTATATTGTCATCATAGATGAA 1328
```

Db 149 GTTAAATGTTACTTTTATCTCCACCATAGATATGGTATTAACAAAGGGTTGGTAA 208
QY 1329 TTCATCGACGAATGCAA 1345
Db 209 TTCATTGACAGAACAA 225

RESULT 9
US-09-925-065A-311017/c
; Sequence 311017, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 311017
; LENGTH: 634
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-311017

Query Match 2.4%; Score 34.2; DB 6; Length 634;
Best Local Similarity 52.6%; Pred. No. 1.8;
Matches 72; Conservative 1; Mismatches 64; Indels 0; Gaps 0;
QY 1209 ATGGAACGTCCTCCACCTGGACGGAACAGTATCCACTGTAAACCCCTGGCTCGTTTT 1268
Db 163 ATAAGAAGGTAACTCTGCTGGAAGGAAGTACCATGCTCTTTTCTGTTCATGATAT 104
QY 1269 ATCCGATTTCTGTTTCGCAATCAGCTTGGTATATTCATGTCATCATAGATGAA 1328
Db 103 GTTAAATGTTACTTTTATCTCCACCATAGATATGGTATTAACAAAGGGTTGGTAA 44
QY 1329 TTCATCGACGAATGCAA 1345
Db 43 TTCATTGACAGAACAA 27

RESULT 10
US-10-467-657-5805
; Sequence 5805, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5805

; LENGTH: 810
; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5805
Query Match 2.4%; Score 33.8; DB 8; Length 810;
Best Local Similarity 51.7%; Pred. No. 2.7;
Matches 77; Conservative 0; Mismatches 72; Indels 0; Gaps 0;
QY 191 GAATATTCACCTCGGACGCTATATGTCGCCCTCCCGATCTATCGCGCGCGAGATGAA 250
Db 21 GAATTTTCCGTCGGTTCGCTGATTTTGGCGCGAGGTTGAGGAAGCCGTTTCATCGCGT 80
QY 251 GTCTGCTTCCGCCCGACCTTCGAAACGTAGTGGCGCGCGCACCATTTTCGGGGGAGAC 310
Db 81 GTATGCGTTTGACGACGCGGACGATATGCGGACGAGGCGAGTATGCCGCTCTGAAGC 140
QY 311 GTCGATGCGCGTGTAAATCAGTTTGAAGC 339
Db 141 CAGGTTGTCGGGTTGGAGGGTTTTCGCGC 169

RESULT 11
US-09-925-065A-268675
; Sequence 268675, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 268675
; LENGTH: 535
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-268675

Query Match 2.4%; Score 33.6; DB 6; Length 535;
Best Local Similarity 57.7%; Pred. No. 2.6;
Matches 60; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
QY 1291 TCACGCTTGGTATATTCATGTCATAGATGAATTCATCGACGAATCAATCAGG 1350
Db 350 TCATTCTTGTATATCTCAACTAAATCAGAGTTGAGGAACCCAGGGGAAATGCACCTCAGG 409
QY 1351 TCAAAATATCCTCGGCAAGGTATGTAATTTGAAACAATCGC 1394
Db 410 GCATATCATATTGCTCCAGAGATGTAATTTCTCTGCAACCTGCGC 453
RESULT 12
US-09-925-065A-585978
; Sequence 585978, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135

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; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 585978
; LENGTH: 388
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-585978

Query Match          2.4%; Score 33.4; DB 6; Length 388;
Best Local Similarity 49.2%; Pred. No. 2.7;
Matches 88; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

QY 1075 TCTTCGAGTAATCGGCGCGGAGCCAGTCAGCGATCTCCGCAAAATGAGCGCGCGCTG 1134
Db      |||||
QY 143 TCGCCGTGTGTCATGGAGGAGCCAGTCAGAGGTGATTGAATCATGCGGGGTGTTTC 202
Db      |||||
QY 1135 TAGTTGAATTTAGTGCCTCCGCGCGGCTTTTCGCCCAATCGGTCCGTCGATCAGCGTC 1194
Db      |||||
QY 203 TCGTGTCTCTCATGATAGTAGTGAGTTCATCATGAGATCTGATGATTTTATAGCTAC 262
Db      |||||
QY 1195 TCACGTATCTTTTGATGAAACGTCCTTCACCTGTGACGGGAACAGTTATCCACTGTAA 1253
Db      |||||
QY 263 TGGCATTTCCCTGTGTGGCACTTATCTCTCCCTTTCTCTTATAAATTACCCAGTCTGA 321
Db      |||||

RESULT 13
US-09-925-065A-411236
; Sequence 411236, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 411236
; LENGTH: 613
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-411236

Query Match          2.4%; Score 33.4; DB 6; Length 613;
Best Local Similarity 57.0%; Pred. No. 3.2;
Matches 61; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 540 TCGTGTGCTTCCCGCCTGAAGAGTCCTCAGCATTTGTGTGTGGGCGTCGTCGCTG 599
Db      |||||
QY 215 TCAGGCACTGCATACATAAATATACATCACTTTTGTGTGTGTGTGTGTGTGTGTG 274
Db      |||||

; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 585978
; LENGTH: 388
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-585978

Query Match          2.4%; Score 33.4; DB 6; Length 388;
Best Local Similarity 49.2%; Pred. No. 2.7;
Matches 88; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

QY 1075 TCTTCGAGTAATCGGCGCGGAGCCAGTCAGCGATCTCCGCAAAATGAGCGCGCGCTG 1134
Db      |||||
QY 143 TCGCCGTGTGTCATGGAGGAGCCAGTCAGAGGTGATTGAATCATGCGGGGTGTTTC 202
Db      |||||
QY 1135 TAGTTGAATTTAGTGCCTCCGCGCGGCTTTTCGCCCAATCGGTCCGTCGATCAGCGTC 1194
Db      |||||
QY 203 TCGTGTCTCTCATGATAGTAGTGAGTTCATCATGAGATCTGATGATTTTATAGCTAC 262
Db      |||||
QY 1195 TCACGTATCTTTTGATGAAACGTCCTTCACCTGTGACGGGAACAGTTATCCACTGTAA 1253
Db      |||||
QY 263 TGGCATTTCCCTGTGTGGCACTTATCTCTCCCTTTCTCTTATAAATTACCCAGTCTGA 321
Db      |||||

RESULT 14
US-09-925-065A-279367/c
; Sequence 279367, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 279367
; LENGTH: 1194
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-279367

Query Match          2.4%; Score 33.4; DB 6; Length 1194;
Best Local Similarity 53.4%; Pred. No. 4.2;
Matches 70; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 1261 CTCGTTTTGATCCGATCTTCTTCGCCCAATCACCTTGGTATATTTGCAATGTCATCATAG 1320
Db      |||||
QY 950 CTCCTTTCTGGAATCATCTGCTGTATAAAATAACAGGAGTGATTTTTCATACAGCAAG 891
Db      |||||
QY 1321 ATGATGAATTCATCGACCAATGCATCAGTCAAAATATCTCGCAAGGTATGTAATTT 1380
Db      |||||
QY 890 ATGATAAAACAAGTTAGTAAAGAAATAAGGTCAAAATAATATTTATTAATTTGTCATAT 831
Db      |||||
QY 1381 GATTGAACAAT 1391
Db      |||||
QY 830 GGTTTAATAAT 820
Db      |||||

RESULT 15
US-10-750-185-707
; Sequence 707, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 707
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; LENGTH: 600
; TYPE: DNA
; ORGANISM: Bovine MMBT09508
US-10-750-185-707

Query Match      2.4%; Score 33.2; DB 8; Length 600;
Best Local Similarity 61.6%; Pred. No. 3.7;
Matches 53; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 1298 TGGTATATTGCATGTCATCATAGATGATGAATTCATCGACGCAATGCAATCAGGTCAAAAT 1357
Db 139 TGGAAATCTGCATGTAGTATTAATAAAAAACATTATCTTGAACATGCGCATCAGGAAAAAT 198

QY 1358 ATCCTCGCCAAGGTATGTAATTTGAT 1383
Db 199 ATACCCCTGGAAGATGTGAATTTAAT 224

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Search completed: February 20, 2006, 02:42:19
Job time : 461.429 secs

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